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ALIGNMENTS

	ORIGIN	BASE COUNT	SOUTCE	CONTRACTOR	FEATTRES	JOURNAL		TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	NID	ACCESSION	DEFINITION	LOCUS	I32406	RESULT 1
•		175 a 182 c 190 g 164 t	\Organism="iinknows"	1 711	Tocation /Onalifiers	Patent: US 5587458-A 1 24-DEC-1996:	diagnostic uses thereof	Anti-erbB-2 antibodies, combinations thereof, and therapeutic and	King, C.Richter, Kasprzyk, P.G. and Bird, R.E.	1 (bases 1 to 711)	Unclassified.	Unknown.	Unknown.	•	g1823197	I32406	Sequence 1 from patent US 5587458.	I32406 711 bp DNA PAT		
				•				and therapeutic and										07-JAN-1997		

Query Match

98.3%; Score 699.6; DB 6; Length 711;

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                     Batra, J.K., Kasprzyk, P.G
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Proc. Natl. Acad. Sci. U.
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Vertebrata;
GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 108547] from the original journal article. This sequence comes from Fig. 1.
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HGKNLEWIGLINPYNGDTNYNQKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCAR
RVTDWYFDVWGAGTTVTVS"
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Ekida,T., Yasukawa,K., Imanaka,T. and Takagi,M.
PRODUCTION OF SINGLE-STRAND FV ANTIBODY
Patent: JP 1997220092-A 2 26-AUG-1997;
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pr 1997220092-A/2
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Shinamura,T., Hamuro,J., Nakazawa,H., KaTakeshita,T.
Monoclonal antibodies which bind the gan interleukin-2 receptor
Patent: US 5582826-A 1 10-DEC-1996;
Location/Qualifiers
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21-APR-1994 JP 1994082836
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SHIMAMURA TOSHIAKI, HAMURO JUNJI, NAKAZAWA HARUMI,
KANAYAWA YUKA,
SUGAMURA KAZUO, TAKESHITA TOSHIICHI
C12P21/08,AG1K39/395,AG1K39/395,C12N1/21,C12N5/20,
C12N15/13/C12N15/06,
C12P21/08,C12R1:19),(C12P21/08,C12R1:91),(C12N1/21,C12R1:19);
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/cell_type="hybridoma"
/cell_line="GP-2"
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/product="anti-IL-2 rece
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                                                                                                                                                                                                                                                                                                                                                        Score 434; DB 27;
Pred. No. 2.2e-123;
1; Mismatches 136;
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King, C.Richter, Kasprzyk, P.G. and Bird, R.E.
Anti-erbB-2 antibodies, combinations thereo
diagnostic uses thereof
Patent: US 5587458-A 2 24-DEC-1996;
Location/Qualifiers
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Unclassified.
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Pred. No. 1.1e-119;
1; Mismatches 131;
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Best Local Similarity 71.9
Matches 537; Conservative
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1 (bases 1 to 916)

Ledbetter, J. A., Gilliland, L.K., Hayden, M.S., Linsley, P.S., Bajorath, J. and Fell, H. Perry.

Expression vectors encoding bispecific fusion proteins and of producing biologically active bispecific fusion protein
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Location/Qualifiers
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Pred. No. 2.3e-99;
0; Mismatches 173;
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*AGACTACATGGAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG
                                   TAACTACAACCAGAAGTTCAAGGGCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCAC
                                                                                                                   GAAGATATCCTGCAAGGCTTCTGGTTACTCACTGGCTACTACATGCACTGCGTGAA
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                                                                                                                                                                                                                               AGGGGGGTCCAAGCTGGAAATAAAAGGTTCTA----CCTCTGGTTCTGGTAAATCTTCTGA 354
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                                                                     GCAGAGCCATGGAAAGAACCTTGAGTGGATTGGACTTATTAATCCTTACAATGGTGATAC
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                                                                                                                                                                                                                 TGGAGGGACCAAGCTGGAGCTCAAAGTCGAGAAATCCTCAGGATCTGGCTCCGAATCCAA
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Shimamura,T., Hamuro,J., Nakazawa,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3 from 131036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibodies which bind the interleukin-2 receptor Patent: US 5582826-A 3 10-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown
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1 ATGGACCTGCAGCTGACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGGAGAAGGTA 60

Query Match
Best Local Similarity
Matches 519; Conserv

Conservative

48.9%; 71.5%;

; Score 348.4; i; Pred. No. 5.7e
0; Mismatches

.7e-97; les 191;

Indels

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                                                                                                                                                   "IMMUNOSUPPRESSIVE AGENT";
Patent number JP 1995313188-A/2, 05-DEC-1995.
AJINOMOTO CO INC, SUGAMURA KAZUO,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shimamura T., Hamuro J., Takeshita T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA encoding an monoclonal antibody against receptor gamma chain.
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08-OCT-1997
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  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                  Mus sp. (mouse)
JP 1995313188-A/2
05-DEC-1995
21-APR-1994 JP 1994082836
21-APR-1993 JP 93P 94491, 07-MAR-1994 JP 94P
21-APR-1993 JP 93P 94491, 07-MAR-1994 JP 94P
                                                                                                                                                                                                                                                                                                                                SUGAMURA KAZUO, TAKESHITA TOSHIICHI
C12P21/08,A61K39/395,A61K39/395,C12N1/21,C12N5/20
C12N15/13//C12N15/06,
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  BP; 199 A; 169 C;
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                                1. .729
/organism="Mus
                                                                                                     Location/Qualifiers
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52, Last updated, Version
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                                                                                                                                                                                   /organism="Mus sp."
/cell_type="hybridoma"
/cell_line="GP-4"
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RESULT 1
SYNDA44X
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AUTHORS
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                                 Escherichia coli
                                                      artificial sequence.

1 (bases 1 to 744)
Lee,T.K., Rollence,M.L., Hallberg,P.L., Oelkuct,M.
Nagle,J.W. and Filpula,D.R.
Production of engineered IgM-binding single-chain
                                                                                                                               Artificial gene cDNA to mRNA artificial sequence
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                                                                                                                                                              monoclonal antibody.
                                                                                                                                                                            IgM-binding protein; fusion protein;
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                                                                                                                                                                                                                                                                                                                                                                                               TCTCTCACAGTCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGG
 TCTGCAGTCTATTACTGTGCAAGGAGGGTTACGGACTGGTACTTCGATGTCTGGGGCGCA 69:
                                                                                                                   ACTGTAGACAAGTCGTCCAGCACAGCCTACATGGAGCTCCTCAGTCTGACATCTGAGGAC
                                                                                                                                                                                                                     TTTGTGAAGCCTGGGGCTCCAGTGAAACTGTCCTGCCAAGGCTTCTGGCTACCCTTCACC
                                                                                                                                                                                                                                                                                              GTGGTGAAGCCTGGAGGTTCAATGAAGATATCCTGCAAGACTTCTGGTTACTCATTCACT
                                             TCTGCGGTCTATTACTGTGCAAGGGAAACTTATGATTACCCCCTTTGCTTACTGGGGCCCAA
                                                                                                      ACTGTGGACAAATCCTCCAGCACAGCCTACATCCAACTCAGCAGCCTGACATCTGAGGAC
                                                                                                                                                              ATTGATCCTTACGATAGTGAAACTCTCTACAATCAAAAGTTCAAGGACAAGGCCACACTG
                                                                                                                                                                               ATTAATCCTTACAATGGTGATACTAACTACAACCAGAAGTTCAAGGGCAAGGCCACATTT
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382. .744
/note="variable heavy chain d
/note="variable heavy chain d
antibody DA4.4 (ATCC HB57)"
a 187 c 186 g 179 t
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VNWMKQRPGRGLEWIGRIDPYDSETLYNQKFKDKATLTVDKSSSTAYIQLSSLTSEDS
ANYYCARETYDYPFAYMGQGTLVTVS"
1 22n
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/db_xref="taxon:29278"
<1. .735
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Pred. No. 9.2e-94;
1; Mismatches 166;
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Length Indels

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                              TAAAGGTGTGCAGCTGCAGGAGTCAGGACCTGAGGTGGAAGCCTGGAGGTTCAATGAA
                                                                                    GGGGTCCAAGCTGGAAATAAAA---GGTTCTACCTCTGGTTCTGGAAATCTTCTGAAGG
                                                                                                                                         AGGATCCTCCCCCAAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGC
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                                                                  GGGGACCAAGCTGGAGCTCAAAGAGGGTAAATCCTCAGGATCTGGCTCCGAATCCAAAGT
                                                                                                                         TGAAGATGTTGCCACTTATTACTGTTTTCAGGGGAGTGGGTACCCCGTACACGTTCGGAGG
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1 (bases 1 to 738)
1 (bases 1 to 738)
1 (bases 1 to 738)
2 (baudhary, V.K., Batra, J.K., Gallo, M.G., Willingham, M.C., Fitzgerald, D.J. and Pastan, I.

Fitzgerald, D.J. and Pastan, I.

A rapid method of cloning functional variable-region antibody in Escherichia coli as single-chain immunotoxins

Proc. Natl. Acad. Sci. U.S.A. 87, 1066-1070 (1990)
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/note="linker DNA"
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/db_xref="taxon:29278"
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           GGCCACACCATGAACTGGGTGAAGCAGAGCCATGGAAAGAACCTTGAGTGGATTGGACTT
                                                                    GTGGTGAAGCCTGGAGGTTCAATGAAGATATCCTGCAAGACTTCTGGTTACTCATTCACT
                                                                                                                         GGTTCTGGTAAATCTTCTGAAGGTAAAGGT---GTGCAGCTGCAGGAGTCAGGACCTGAG
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GACCATGCAATTCACTGGGTGAAACAGAACCCTGAACAGGGCCTGGAATGGATTGGATAT
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unknown.
Unclassified
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47; Conservative
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Pred. No. 6.7e-88;
1; Mismatches 161
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TITLE
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Best Local Similarity
Matches 416; Conserv
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                                 GACCATGCAATTCACTGGGTGAAACAGAACCCTGAACAGGGCCTGGAATGGATTGGATAT
                                              GGCCACACCATGAACTGGGTGAAGCAGAGCCATGGAAAGAACCTTGAGTGGATTGGACTT
                                                                                       GTGGTGAAGCCTGGAGGGTTCAATGAAGATATCCTGCAAGACTTCTGGTTACTCATTCACT
                                                                                                                                  GGTTCTGGTAAATCTTCTGAAGGTAAAGGT---GTGCAGCTGCAGGAGTCAGGACCTGAG
                                                                                                                                                                             AGTCGTAGCCCACCCACGTTCGGAGGGGGGGTCCAAGCTGGAAATAAAAGGTTCTACCTCT
                                                                                                                                                                                                             ACTCTCTCCATCAGCAGTGTGAAGACTGAAGACCTGGCAGTTTATTACTGTCAGCAGTAI 360
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ATTAATCCTTACAATGGTGATACTAACTACAACCAGAAGTTCAAGGGCAAGGCCACATTT
                                                                                                                                                                 TATAGCTATCCCCTCACGTTCGGTGCTGGGACCAAGCTTGTGCTGAAAGGCTCTACTTCC
                                                                                                                       GGTAGCGGCAAATCCTCTGAAGGCAAAGGTCAGGTTCAGCTGCAGCAGTCTGACGCTGAG
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Sequence
AR012824
g3971142
                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 803)
Whitlow,M., Filpula,D. and Shorr,R.
Antigen-binding fusion proteins
Patent: US 576373-A 7 09-JUN-1998;
Location/Qualifiers
1. 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unknown.
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Best Local S
Matches 499
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                                              TGCTCGCTTCAGTGGCGGTGGGTCTGGGACCTCTTACTCTCTCACAGTCAGCAGAGTGGA 237
                                                                                            GCCAGGATCCTCCCCCAAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCC
                                                                                                                            TATCACCTGCAGTGCCAGCTCAAGTATAAGTTCCAATTACTTGCATTGGTATCAGCAGAA 125
                                                                                                                                                   AATGACTTGCAGGGCCACCCCAAGTGTAAG-----TTACATGCACTGGTATCAGCAGAA 117
                                                                                                                                                                          GACATTCAGCTGACCCAGTCTCCAACCACCATGGTTGCATCTCCCGGGGGAGAAGAT-CAC
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             GCCAGGATTCTCCCCTAAACTCTTGATTTATAGGACATCCAATCTGGCTTCTGGTGTCCC
MASAHIRO
PC C12N
PC C12R
PC C12R
CC Stra
CC topo
CC hypo
CC anti
FH Key
FH Sour
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Ekida,T., Yasukawa,K., Imanaka,T. and Takagi,M.
PRODUCTION OF SINGLE-STRAND FV ANTIBODY
Patent: JP 1997220092-A 1 26-AUG-1997;
TOSOH CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF PR OC S
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DNA encoding
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JP 1997220092-A/1
26-AUG-1997
15-FEB 1996 JP 1996027622
EKIDA TEIJI, YASUKAWA KIYOSHI, IMANAKA TADAYUKI,
                                                                                                                                                                                                                                                                                                                                                                                                  topology: Linear;
hypothetical: No;
anti-sense: No;
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Location/Qualifiers
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/db_xref="taxon:32644"
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y a single
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Pred. No. 6.5e-87;
1; Mismatches 208;
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anti-T3 antibody TTl.
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Best Local Similarity 69.8
Chas 469; Conservative
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                                          GAAGCCAGGATCCTCCCCCCAAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGT
                                                                             CACCATGACCTGCAGGGCCAGCTCAAGTGTAAGTTCCAGTTACTTGCACTGGTTCCAGCA 119
                                                                                                CACAATGACTTGCAGGGCCACCCCAAGTGTA-----AGTTACATGCACTGGTATCAGCA 114
                                                                                                                                                   ATGGACCTGCAGCTGACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTA
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                            GAAGTCAGGTGCCTCCCCCAAACTCTGGATTTATAGCACATCCAACTTCGCTTCTGGAGT
                                                                                                                                      ATGGAAAATGTGCTCACCCAGTCTCGAGCAATCATGTCTGCATCTCCAGGGGAAAAGGT-
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                                                                                                                                                                                                                                                                                                 1 (bases 1 to 741)
Ladner,R.C. and Bird,R.E.
SINGLE POLYPEPTIDE CHAIN BINDING MOI
PATENT: WO 8801649-A 10 10-MAR-1988;
Location/Qualifiers
1. .741
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10 from Patent WO 8801649.
108678
9588616
                                                                                                                                                                                                                                                                                                                                                                                                 Unknown.
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188 c 192 g
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Pred. No. 4.1e-86;
0; Mismatches 193;
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                                                                                                                                                                                           Indels
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Search completed: May 13, 1999, 09:54:13 Job time: 1170 sec

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Result
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AA691311
AA592800
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AA592800 vo25g11.r
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ALIGNMENTS

COMMENT	TITLE	REFERENCE AUTHORS	NID KEYWORDS SOURCE ORGANISM	LOCUS DEFINITION ACCESSION	AA691311
Unpublished (1996) Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP	Schellenberg, K., Steptoe, M., Tan, F., Materia, M., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R. The WashU-HHMI Mouse EST Project	Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 396) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel S. Kucaba T. Lacv M. Le M. Martin T. Morris M.	92692247 EST. house mouse. Mus musculus	AA691311 396 bp mRNA EST 16-DEC-1997 vs14f01.rl Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone 1138201 5' similar to 9b:X67211 M.musculus rearranged immunoglobulin kappa light chain (MOUSE);, mRNA sequence. AA691311	

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RESULT
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                                                                                                                                                           AA592800 344 bp mRNA EST 17-SEP-1997 vo25911.r1 Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone 1050980 5' similar to gb:x67211 M.musculus rearranged immunoglobulin kappa light chain (MOUSE);, mRNA sequence.

AA592800
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 344)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
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Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                Mus musculus
                                                                                                                                              g2406463
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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/dev_stage="8 weeks"
/lab_host="DH10B"
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/strain="FVB/N"
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UIN

AI180569 310 bp mRNA EST UB-UCIT-1990 UC70f09.rl Soares mouse mammary gland NDMMG MUS musculus cDNA clone uc70f09.rl Soares mouse mammary gland NDMMG MUS musculus cDNA clone 1431017 5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); gb:M12376 Mouse immunoglobulin H-chain V-region pseudogene

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BASE CO
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                                                                             GCGGTGGGTCTGGGACCTCTTACTCTCTCACAGTCAGCAGAGTGGAGGCTGAAGATGCTG
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CCACTTATTACTGCCAGCATTGGAGTAGTA
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Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Theising, B., Wylie, T., Waterston, R.
The WashU-HHMI Mouse E
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                     Conservative
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adaptors [AATTCGGATCCTTG], digested with Not I and clone
into the Not I and Eco RI sites of the modified pT7T3
vector. Library constructed by Bob Barstead."
/db_xref="taxon:10090"
/clone="1050980"
/clone="1050980"
/clone="11b="Barstead mouse irradiated colon MPLRB7"
/dev_stage="8 weeks"
/lab_host="DH10B"
/1.>344
91 c 70 g 92 t
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/strain="FVB/N"
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83.7%;
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                                                                                                                                                                                                                                                                                                     CACTGGCCACACCATGAACTGGGTGAAGCAGAGCCATGGAAAGAACCTTGAGTGGATTGG 507
                                                                                                                                                                                                                                                                                                                                                                                          TAAGCTTGTGAAGCCTGG-GGTTCAGTGAAGCTGTCCTGCAAGGCTTCTGGCTACACCTT 84
                                  ATTTACTGTAGACAAGTCGTCCAGCACAGCCTACATGGAGCTCCTCAGTCTGACATCTGA 627
                                                                                                                                                                                           ACTTATTAATCCTTACAATGGTGATACTAACTACAACCAGAAGTTCAAGGGCAAGGCCAC 567
                                                                                                                                                                                                                                                            CACCAGCTACTGGATGCAGTGGGTAAAAACAGAGGCCTGGACAGGGCATTGAGTGGATCGG 144
AGAGATTGATCCTTCTGATAGCTATACTAACTACAATCAAAAGTTCAAGGGCAAGGCAGC
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93731207
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Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL;
This clone is available royalty free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of MedicineP
4444 Forest park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
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Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
77 c 85 g 67 t
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/clone="1431017"
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/strain="C57BL/6J"
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Sciurognathi; Muridae; Murinae;
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79.88;
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Pred. No. 2.1e-44;
0; Mismatches 54
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Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Trace considered overall poor quality
Seq primer: -28m13 rev2 ET from Amersh
High quality sequence stop: 1.
[ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston, R.
The WashU-HHMI Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                 /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
a 68 c 77 g
                                                                                                                                                   /sex-"male"
                                                                                                                                                                     /clone_lib="Soares 2NbMT"
 22.8%;
76.7%;
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Score 162.4; DB Pred. No. 7e-41;
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                 DB 28;
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RESULT 5
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                                                                       Matches 210;
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435 GTGCAGCTGGTGCAGTCTGGGGGCTGAGGTGAAGAAGCCTGGGGGCCTCAGTGAAGGTCTCC 376
                  365 GTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTGGAGGCTGGAGGTTCAATGAAGATATCC 424
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI201426 461 bp mRNA EST 30-OCT-1998 qs73c06.xl NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:1943722 3' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); contains Alu repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert Length: 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 461)
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National Cancer Institute, Cancer Genome Anatomy
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Location/Qualifiers
                                                                                                                                                                                93
                                                                       Conservative
                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr2 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-98679, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
/db_xref="taxon:9606"
/clone="IMAGE:193722"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Robert_Strausberg@nih.gov
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                                                                                                                                                                                             /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                  /sex="male"
                                                                                                                                                                                                                                                   /clone_lib="NCI_CGAP_Pr28"
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72.4%;
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 387)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
AA569186
                                                                                                                                                                                                                                                                                                               Insert Length: 1722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                     found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email:
                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: David B. Krizman, Ph.I. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                   89
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                                                                                                                                                     /note-"Vector: pamp10; mRNA made from liposarcoma, of made by oligo-dT priming. Non- directionally cloned Size-selected on agarose gel, average insert size (Reference: Krizman et al. (1996) Cancer Research
                                              /clone="IMAGE:1061683"
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/lab_host="DH10B"
                                                                                                                                          56:5380-5383.
                                                                                                                                                                                                                           /organism="Homo sapiens"
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EST.
                                                                                                                                                                                                                                                                                                                                          Fax: 514 200 10.10
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
This clone is available royalty-free through LLNL;
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AA710291
                                                                                                                                                                                                                                                                                                                               IMAGE Consortium (info@image.linl.gov)
MGI:632678
                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu Marra, M., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
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adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead." /db_xref="taxon:10090" /clone="1166766"
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/strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTTCAGTGGCGGTGGGTCTGGGACCTCTTACTCTCTCACAGTCAGCAGAGTGGAGGCTG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATCCTCCCCCAAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGCTC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCACCTGCAAGCCAGTCAGAATGTGGGTACTAATGTAGCCTGGTATCAAGAGAAACCAG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATGACTTGCAGGGCCACCCCAAGT-GTAAGTTACATGCACTGGTATCAGCAGAAGCCAG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACATTGTGATGACCCAGTCTCAAAAATTCATGTCCACATCAGCTGGAGACAGGGTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTCCAAGCTGGAAATAAAA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGACCAAGCTGGAAATAAAA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCAATCTCCTAGAGCACTGATTTACTCGGCATCCTACCGGTACAGTGGAGTCCCTGATC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGACTTGGCAGAGTATTTCTGTCAGCAATATAACAGCTTTCCGTACACGTTCGGAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATGTGCAGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206;
                                                                                                                                      Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Ix
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA710970 431 bp mRNA EST 24-DEC-1997 vt93h09:rl Soares mouse mammary gland NDMMG MUS mUSCULUS CDNA clone 1178753 5' similar to gb:m18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); gb:x70423 M.musculus mRNA for monoclonal antibody heavy chain gamma (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 431)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free
IMAGE Consortium (info@image.llnl.go
                                                                                                                                                                                                                                                                    Unpublished (1996)
                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse
                                                                                                                                                                                                                                                                                                       Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                    MGI:636601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                               primer: -28m13 rev2 ET from Amersham
h quality sequence stop: 198.
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/dev_stage="8 weeks"
/lab_host="DH10B"
81 c 88 g
             try sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                            e; Metazoa; Chordata; Vertebrata;
Sciurognathi; Muridae; Murinae; M
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                                                                                                                                                                                                                                                                                     EST Project
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                                                                                   .gov)
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                                                                                   through LLNL
v) for further
                                                                                                                                                                           Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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SOURCE
ORGANISM
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ORIGIN
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Best Local S
Matches 188
                                                                                                                                                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCAGCTGCAGGAGTCAGGACCTGAGGTGGTGAAGCCTGGAGGTTCAATGAAGATATCCT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGATCAACCACCAAAAATGAGGACACGGCTACATATTTCTGTGCCCCCAATACTTTCTA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGACTTCAAGGGACGGTTTGCCTTCTTTTGGAAACCTCTGCCAGCACTGCCTATTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAAGTTCAAGGGCCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCACAGCCTACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAAGGGTTTAAAGTGGATGGGCTGGATAAACACCTACTCTGGAGTGCCAACATATGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                    9609691
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST100653 Homo Sapiens CDNA 5' end similar to immunoglobulin light chain, V region (GB:L01279) (HT:3043).
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Godayne, J.D., White, O., Sutton, G., Bladke, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,
                                                                                                                                                                                                                  Deuterostomia; Chordata; Vertebrata; Gnathostomata; Os
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; H
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                       Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                                                                                                                                                                                                                               human primer=Ml3 Reverse library=Human Pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             668
                                                                                                                                                                                     (bases 1 to 393)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
/strain="C57BL/6J"
/note="Organ: mammary gland; Vector: pT7T3D-Pac
/note="Organ: mammary gland; Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I -
oligo(dT) primer [5'
olig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
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/clone="1178753"
/clone_lib="Soares mouse mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
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62.0%;
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Pred. No. 3.6e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 g
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                                            KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GACCTGCAGCTGACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTACAC 63
                                                                                                                                                                                                                                                                                             TGAAGATGCTGCCACTTATTACTGCCAGCAGTG-GAGTCGTAGCCCACCCACCGTTCGGAG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATGACTTGCAGGGCCACCCCAAGTGTAAGTTACATGC---ACTGGTATCAGCAGAAGCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGATCCTCCCCCAAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTCACTTGCCGGGCAAGTCAGAGCATTAGCACCTTTTTAAATTGGTATCAGCAGAAACC 171
                                                                                                                                                                                                                                                                                                                                         GGGGGTCCAAGCTGGAAATAAAAGGTTCT
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                                                                                                                                                                                                                                                                                                                                                                                     TGAAGATGTTGCAACTTACTACTGTCAACAGAGTTNCACTTATGNCTCGGACGGTTGGCC
                                         (HUMAN);,
AA291381
g1939359
EST.
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                                                                                                          AA291381 379 bp mRNA EST 08-AUG-1997 zt44902.rl Soares ovary tumor NDHOT Homo sapiens cDNA clone 725234 5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20
Tel: 301869905
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1995)
Other_ESTs: THC24356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: tdbinfo@tdb.tigr.org
For clone availability, addinformation related to this
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Pred. No. 4.7e-27;
1; Mismatches 107;
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Best Local
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                                                                                       273
                                                                                                                                                                                         543 ACCAGAAGTTCAAGGGCCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCACAGCCTACA
                                                                                                                                                                                                                                                             423 CCTGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCC 482
                                                                                                                                                        213 CAGGGAGTTTTCAGGACAGAGTCAGCTTGACCACTGACACATCCACGAATACAGCCTACA
                                                                                                                                                                                                                                                                                                                                                                                                       363 GTGTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTGAAGCCTGGAGGTTCAATGAAGATAT 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                     TGGAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG 654
                                                                                   TGGAGCTGAGGAACCTGAGATCTGACGACACGGCCATATATTACTGTGCGAG
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
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Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
 AA318377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Female"
/tissue_type="ovarian tumor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="725234"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B (ampicillin resistant)"
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                                                                                                             118 GCCAGGATCCTCCCCCAAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCC 177
178 TGCTCGCTTCAGTGGCGGTGGGTCTGGGACCTCTTACTCTCTCACAGTCAGCAGAGTGGA 237
                                                                        62
                                                                                                                                                                                                                                                                             61 CACAATGACTTGCAGGGCCACCCCAAG---TGTAAGTTACATGCACTGGTATCAGCAGAA 117
                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                           CACCATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTACATTGGTATCAGCACAA 61
                                                                     ACCAGGTAAAGCCCCTAAACTCCTGATCTATGNTACATCCACTTTGCAAAGTGGGGTCCC
                                                                                                                                                                                                                                                                                                                                                     182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, Meldman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Raymond, L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Frieder, J., Fields, C., Frieder, C., Haseltine, W.A., Fields, C., Frieder, C., Haseltine, W.A., Fields, C., Frieder, C., Fields, C., Frieder, C., Fields, C., Frieder, C., Fields, C., Frieder, C., 
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AA318377
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The Institute for Genomic
9712 Medical Center Drive,
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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Eukaryotae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: arkerlav@tigr.org
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<1..>335
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ECORI; Site_2: Xho!"
/db_xref="ATCC (inhost):119058"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
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                                                                                                                                                                                                                                                                                                                                                                               16.3%;
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Pred. No. 2.0
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nes 92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnebm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrick, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Welsmer, P. S., Olsen, H., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Welsmer, P. S., Olsen, H., Raymond, L., Wel, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 8 million nucleotides of CDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAAGGGNCCAAGGTGGCAATCAAACGNACTGTGGCTG
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96026280
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Kerlavage, AR
Bioinformatics
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                                                                                                                                                                                     For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
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                                                                                                                                                                                                                                                                                                                                                     Email: arkerlav@tigr.org
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Ho
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                                                                                                                           /note="Organ: testis; Vector: pBluescript SK-;
ECORI; Site_2: XhOI"
/db_xref="ATCC (inhost):191658"
/db_xref="taxon:9606"
                                                                                   /sex="male"
                                                                                                      /clone_lib="Testis tumor"
                                                                                                                                                                                                        /organism="Homo sapiens"
                                                           dev_stage="adult"
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Query Match
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or83g01.s1 |
similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
AA987559
g3172923
                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 336)
10CI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy ProTumor Gene Index
                                                                                                          CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST
Insert Length: 801 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 322.
Location/Qualifiers
                                                                                                                                                                                                                                            Tissue Procurement: Chri
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
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5 gb:M87789
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Pred. No. 1.
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Homo sapiens cDNA clone IMAGE:1602480
GAMMA-1 CHAIN C REGION (HUMAN);, mRNA
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.2e-25;
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/note="Organ: lung; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated

/organism="Homo sapiens"

to Eco RI adaptors (Pharmacia), digested with Not

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BASE COUNT
ORIGIN
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  JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32
                                                              Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Cliayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dinke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGAAGTTCAAGGGCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCACAGCCTACATG 604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCCAGATAGAACAGTCAGGGGCTGAGGTGAAGAAGCCAGGGTCTTCGGTGAAGGTCACC 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
AA345486
g1997722
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EST51505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA345486 403 bp mRNA EST 21-APR-1997 EST51505 Gall bladder II Homo sapiens cDNA 5' end similar to similar to immunoglobulin kappa light chain, V region (GB:X06
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae;
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/clone="IMAGE:1602480"
/clone_lb="WcI_CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, Library was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kerlavage, A.R., Fleischmann, R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mitochondrial eukaryotes; Metazoa; Chordata; Mamumalia; Eutheria; Primates; Catarrhini; Ho
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Best Local
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 CTCCAGGGGAGAAGGTACACAATGACTTGCAGGGCCACCCCAAGTGT-----AAGTTAC 97
                                                                                                                                                                                                                                                                                                                                                                          15
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                                                                                                                                                                                                                                                                                                                                                                                                                                GACTCACCTAGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGTAGCCCACCCACGTTCGGAGGGGGGGTCCAAGCTGGAAATAAAAGGTTCTACCTCTG 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCACAGTCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGT 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGT 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACT 218
                                                                                                                                                                                                                                    AA423447 398 bp mRNA EST 16-OCT-ve80a03.rl Soares mouse mammary gland NbMMG Mus musculus 832492 5' similar to gb:M63438 IG KAPPA CHAIN PRECURSOR V REGION (HUMAN); gb:M35669 Mouse Ig aberrantly rearranged kappa-chain mRNA V-J2-C-region, (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: arkerlav@tigr.org
For clone availability, additional sequence and ex
information related to this EST, please check the
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                             Bukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Euther; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 398)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubugeisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockvill
                                                                                                                                                                                                                       g2102360
                                                                                                                                                                Mus musculus
                                                                                                                                                                                  house mouse.
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WashU-HHMI Mouse EST Project
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/note="Organ: gall bladder; Vector:
Site_1: EcoRI; Site_2: XhoI"
/db_xref="ATCC (inhost):147008"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult, 25 yrs" <1. .>403
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/sex="female"
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113 c
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63.1%;
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Pred. No. 1.4e-24;
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he TIGR Human Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 15.6%; Score 110.8; DB 24; Length 398; Best Local Similarity 63.2%; Pred. No. 1.4e-24; Matches 211; Conservative 0; Mismatches 107; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
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                                                                                                                                                                                                                                                                                                          169 TGGAGTCCCTGCTCGCTTCAGTGGCGGTGGGTTCTGGGACCTCTTACTCTCTCACAGTCAG 228
                                                                                                                                                                                                                                                                                                                                                                   109 TCAGCAGAAGCCAGGATCCTCCCCCCAAACCTTGGATTTATACCACATCCAACCTKGCTTC 168
                                                                                                                               289 CACGTTCGGAGGGGGGTCCAAGCTGGAAATAAAA 322
                                                                                                                                                                                             305 TCCTATGGAGGAGGATGATACTACAATGTATTTCTGTCAGCAAAGTAAGGAGGTTCCTCG 364
                                                                                                                                                                                                                                        229 CAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTCGTAGCCCACC 288
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                                                                                                           GACGTTCGGTGGAGGCACCAAGTTGGAAATCAAA 398
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This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
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WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
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Seq primer: -28ml3 rev2 ET from Amersham.
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/tissue_type="mammary gland"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH108"
/ab_host="DH108"
/ab_100 c 102 g 95 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 3']; double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
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/clone="832492"
/clone_lib="Soares mouse mammary gland NbMMG"
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/strain="C57BL/6J"
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Title: Perfect score:

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Scoring table:

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240622 seqs, 94065609 residues

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V63620 Q45604 T31541

330.6.6 331.8.4 331.6.6 331.7.8 331.7.

755100 755100 755100 711728 791615 791615 791615 701611 705101 706111 706111 7073679 7129058 7129059

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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OVB3 light and hea
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C The present cDNA sequence codes for a claimed single-chain antibody e23

C designated e23(FY), which binds to erbB-2. Monoclonal antibody e23

C was generated by immunising mice with N/erbB-2 cells overexpressing the gpl85 protein, removing spleen cells and producing hybridomas by standard techniques. Messenger RNA coding for the anti-erbB-2 monoclonal antibody was isolated and converted to cDNA. Regions coding for the heavy- and light- chain variable regions were then amplified by PCR and joined via a sequence encoding a peptide linker. The resulting single-chain antibody is useful for in vitro diagnosis of tumour cells which overexpress the erbB-2 gpl85 marker, e.g. breast, ovarian and non-small cell lung carcinomas, and, when coupled to a cytotoxic agent, to treat such tumours. Sequence 711 BP; 175 A; 182 C; 189 G; 164 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 711
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07-OCT-1991; 772270.
07-OCT-1991; US-772270.
30-JUN-1992; US-906555.
14-MAY-1993; US-061092.
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Single chain antibody; variable region; light chain; heavy chain; breast cancer; ovarian cancer; non-small cell lung carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ARON-) ARONEX PHARM INC.
Bird RE, Kasprzyk PG, King
WPI; 97-064831/06.
P-PSDB; W15185.
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06-JAN-1994.
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30-JUN-1992;
                                                                                       gp185
Example; Fig 7; 37pp; English.
The source of human erbB-2 protein for the prodn. of antibodies no and 21 (Q55180/R45442; Q55181/R45443) is a NIH/3T3 cell engineered to express the human erbB-2 protein on its surface (N/erbB-2). Abs no. 21 and 23 are directed against the extracellular domain of gp185 erbB-2. Nude mice manipulated to produce rapidly growing tumours were used in a trial of the efficacy of the Abs. I animals given a combination of the 2 Abs, tumours completely regressed after 11 days.

Sequence 711 BP; 175 A; 183 C; 187 G; 165 T;
                                                                                                                                                                                       21-OCT-1992; U08545.
30-JUN-1992; US-906555.
(NOLE-) MOLECULAR ONCOLOGY INC.
Kasprzyk PG, King CR;
WPI; 94-025878/03.
P-PSDB; R45442.
P-PSDB; R45442.
Z monoclonal antibodies which recognise different epitopes o
                                                                                                                                                                                                                                                                                                                                Sequence enco
                                                                                                                                                                                                                                                                                                                                                    Q55180 standard;
Q55180;
21-JUL-1994 (fi
                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                         monoclonal antibody;
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                                             Conservative
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                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. 171
/*tag= a
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                                           Pred. No. 3.3e
0; Mismatches
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cancer therapy; preve
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3e-176;
les 2;
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   KW gene therapy; ds.

OS Synthetic.

SYnthetic.

PN W09607321-Al.

PD 14-MAR-1996.

PF 23-AUG-1995; U10740.

PF 06-SEP-1994; US-301339.

PR 06-JUN-1995; US-468252.

PA (UABR-) UAB RES FOUND.

CUILED DT, Deshane J;

PI CUILED DT, Deshane J;

PI CHILED T, Deshane J;

PT Inhibition of proliferation or survival of, esp. malignant erbB2, processed and binds, pref. erbB2, protein intracellularly

PT Tells - by introducing nucleic acid mol. encoding antibody homologue

PT which is expressed and binds, pref. erbB2, protein intracellularly

PS Claim 42; Page 29-30; 48pp; English.

CC A nucleic acid comprises a first sequence encoding a signal peptide

CC (R94019) linked to a second sequence (T17728) encoding a single

CC chain FV fragment (R94020) that binds a human erbB2 oncoprotein.

CC The anti-erbB2 SFV portion is obtained by PCR using e23scFV
                                                                                                                                                                                                                        T17728;
21-MAY-1996 (fi:
Anti-erbB2 scFV oncoprotein; erb
intracellular an
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an erbB2 oncoprote.

"R using e Signal pept an erbB2 oncoprote."
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Best Loc
Matches
                    T91615 standard; cDNA to mRN
T91615;
22-DEC-1997 (first entry)
cDNA encoding an anti-gp130
Single chain Fv; scFv; antil
anti-gp130 antibody; inclusi
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid as template. The signal peptide directs the scFv to the endoplasmic reticulum. The nucleic acid is incorporated into a plasmid or viral vector to facilitate expression of the scFv antibor homologue within e.g. an epithelial carcinoma cell. Intracellular expression of the homologue inhibits surface expression of erbB2 an thereby inhibits cell proliferation and cell survival and decreases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing single chain Fv antibody in Escherichia coli - by rexpression in an inclusion body, followed by protein folding or by co-expression with a chaperonin as a soluble fraction claim 4; Page 6-7; 9pp; Japanese.

Claim 4; Page 6-7; 9pp; Japanese.

Chaim 4; Page 6-7; 9pp; Japanese.

Chaim 5; Chaim 6; Chain Fv (scFv)

Cantibodies which are produced in E. coli. The scFv's are derived from an anti-T3 antibody or an anti-1-9p130 antibody and are produced from an anti-T3 antibody or an anti-1-9p130 antibody of Clies. by denaturation and solubilisation) or (2) expression as a soluble fraction by co-expression with chaperonin. Using the methods, coll. by denaturation and solubilisation) or (2) expression or in clusion bodies. Like the parent double chain antibodies, the scFv polypeptides are useful in immunological diagnosis or for separation cand purification, but they lessen the side effects caused by antibody constant regions. The availability of scFv polypeptides contributes or fundamental research and development of diagnostic and therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Sir
Matches 576;
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15-FEB-1996; 027622.
15-FEB-1996; JP-027622.
(TOYJ) TOSOH CORP.
WPI; 97-474306/44.
P-PSDB; W25784.
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Sequence
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CAACCAGAAGTTCAAGGGCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCACAGCCTA
                                                                                                                                                        GTCCAAGCTGGAAATAAAAGGTTCTACCTCTGGTTCTGGTAAATCTTCTGAAGGTAAA---
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                                                                                                     GGACGTCCAATTGCAGCAGTCTGGACCTGAACTGGTGAAGCCTGGGGGCTTCAGTGAAGAT
                                                                                                                                                                                                                         -GGTGTGCAGCTGCAGGAGTCAGGACCTGAGGTGGAGCCCTGGAGGTTCAATGAAGAT
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80.2%;
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No. 6.4e-11
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Best Local Similarity
Matches 574; Conserv
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26-0CT-1994.
21-APR-1994; 106257.
21-APR-1993; JP-094491.
07-MAR-1994; JP-036065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunosuppressant polypeptide - has ability to block interleukin-2 response Claim 17; Page 29; 37pp; English.

MAb capable of binding to the gamma chain of the IL-2 recept thus of blocking the IL-2 response, is produced by mouse hyb line GP-2 (FERM BP-641). DNA encoding the variable region this MAb was expressed in E. coli, yielding Fv(GP-2) with immumosuppressive activity.

Sequence 732 BP; 180 A; 204 C; 182 G; 166 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hamura J, Kanayama
Takeshita T;
WPI; 94-325948/41.
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; monoclonal antibody: hybridoma; interleukin-2;
antibody variable region; GP-2; Fv(GP-2);
                                                                                                              CGGAGGGGGGTCCAAGCTGGAAATAAAAGGTTCTA----CCTCTGGTTCTGGTAAATCTTC
                                                                                                                                                 CACAATGACTTGCAGGGCCACCCCAAGTGTA -----AGTTACATGCACTGGTATCAGCA 114
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               AATGAAGATATCCTGCAAGACTTCTGGTTACTCATTCACTGGCCACCACCATGAACTGGGT
                                                                TGAAGGTAAAGGTGTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTGAAGCCTGGAGGTTC
                                                                                                                                                                                                                                                  GAAGCCAGGATCCTCCCCAAACTCTGGATTATAGCACATCCAACCTGGCTTCTGGAGT
                                                                                                                                                                                                                                                                          GAAGCCAGGATCCTCCCCCAAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGT
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                                                  CAAAAGCACGCAGGTCAAACTCGAGGAGTCTGGATCTGAGCTGGAGGCCTGGAGCTTC
                                                                                                CGGTGCTGGGACCAAGCTGGAGCTCAAAGTCGACAAATCCTCAGGATCTGGCTCCGAATC
                                                                                                                                                                                                                                                                                                   CACCATGACCTGCACTGCCAGCTCAAGTGTAAGTTCCAGTTACTTGCACTGGTACCAGCA
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  AGTGAAGCTGTCCTGCAAGGCTTCTGGCTACACATTCACCAGCTACTGGATGCACTGGGT
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78.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 434;
Pred. No. 1.
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..5e-106;
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 732
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oy mouse hybridoma
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Best Local S
Matches 511
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Q55181;
21-JUL-1994
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06-JAN-1994.
21-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Fig 8; 37pp; English.

Example; Fig 8; 37pp; English.

The source of human erbB-2 protein for the prodn. of antibodies not and 21 (Q55180/R45442; Q55181/R45443) is a NIH/3T3 cell engineered to express the human erbB-2 protein on its surface (N/erbB-2). Abs no. 21 and 23 are directed against the extracellular domain of gp185 erbB-2. Nude mice manipulated to produce rapidly growing tumours were used in a trial of the efficacy of the Abs. animals given a combination of the 2 Abs, tumours completely regressed after 11 days.

Sequence 720 BP; 184 A; 178 C; 179 G; 179 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gp185
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WPI; 94-025878/03.
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Single chain anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treatment of
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(MOLE-) MOLECULAR ONCOLOGY
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PT labels or cytotoxin, useful for detection and treatment of tumour procedules expressing this protein

Example 9; Columns 27-30; 28pp; English.

Character of the present cDNA sequence codes for a claimed single-chain antibody, designated e21(FY), which binds to erbB-2. Monocional antibody e21

Character of the present cDNA sequence codes for a claimed single-chain antibody e21

Character of the present cDNA sequence codes for a claimed single-chain antibody e21

Character of the processing mice with N/erbB-2 cells overexpressing the pp185 protein, removing spleen cells and producing hybridomas composition to the anti-erbB-2

Character of the present expressing for the anti-erbB-2

Character of the heavy- and light-chain variable regions were then coding for the heavy- and light-chain antibody is useful for in vitro linker. The resulting single-chain antibody is useful for in vitro clisher. Each overian and non-small cell lung carcinomas, comparison of the coding a peptide coding single-chain antibody is useful for in vitro clisher. Each coding carcinomas, comparison of the coding and constant cells which overexpress the erbB-2 gp185

CC marker, e.g. breast, overian and non-small cell lung carcinomas, coding and comparison of the coding and carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-DEC-1996.
07-OCT-1991; 772270.
07-OCT-1991; US-772270.
30-JUN-1992; US-906555.
14-MAY-1993; US-061092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-1997 (first entry)
Single-chain anti-erbB2 antibody e21(Fv) cDNA.
Single chain antibody; variable region; light chain; heavy chain; breast cancer; ovarian cancer; non-small cell lung carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bird RE, Kasprzyk PG, WPI; 97-064831/06.
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Expression vector encoding bispecific fusion protein - having binding domains for separate targets joined by helical peptide, and treatment useful e.g. for diagnosis and treatment is Example 1; Fig 11; 50pp; English.

The VL and VH sequences of the anti-CD3 hybridoma G19-4 were amplified by PCR methods. A gene fusion was constructed from the Ct two amplified domains and a (G1945er)3 linker. The amino the Light chain variable region leader peptide and the carboxyterminus was fused directly to the hinge region of the Ccarboxyterminus was fused directly to the hinge region of the Ccarboxyterminus was fused directly to the hinge region of the Ccarboxyterminus was fused directly to the hinge region of the Ccarboxyterminus was fused directly to the hinge region of the Ccarboxyterminus was fused directly to the hinge region of the Ccarboxyterminus was fused directly to the hinge region of the Ccarboxyterminus was fused directly to the hinge region of the FC domain at the Bc11 site and/or to a short "helical" peptide linker to construct the bispecific CD3-L6FvIg antibody derivative. The Ccarboxyterminus constructed in G81076).

Sequence 913 BP; 252 A; 223 C; 228 G; 210 T;
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01-FEB-1993; US-013420.

13-SEP-1993; US-121054.

(BRIM) BRISTOL-MYERS SQUIBB

Bajorath J, Fell PH, Gillil
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                                                                                                     Complete containing a target binding molety capable of binding to a serpin enzyme complex receptor (SECR), and a nucleic acid binding to a complex receptor (SECR), and a nucleic acid binding molety. This can be used in a method for delivering an oligonucleotide to a companian cell. The method comprises conjugating the target binding to a context to form a pharmaceutical composition. A mammalian cell having on its confidence SECR, is contacted with the pharmaceutical composition. A mammalian cell having on its conditions allowing binding to the receptor resulting in delivery of the pharmaceutical composition to the interior of the cell. The composition and method are used for the introduction of exogenous genetic material into target host cells expressing SECR on their surface. The nucleic acid may encode a functional wild-type or mutant gene or may be an antisense composition may comprise a protein partion having therapeutic properties, ce.g. enzymatic activity, cytokine activity and antibiotic activity which is delivered to a cell surface via the SECR binding molety. The nucleic acid can be compacted at high concentrations with the carrier molecule at a critical salt concentration. The condensation of such complexes convoices of the concentration of such complexes and concentration of such complexes are convoices of the concentration. The condensation of such complexes are convoices of the concentration of such complexes are convoices of the concentration of such complexes are convoices of the concentration. The condensation of such complexes are convoices of the concentration of such complexes are convoices of the concentration.
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11-DEC-1997;
03-JUN-1997; U09858.
03-JUN-1996; U3-656906.
(UYCA-) UNIV CASE WESTERN RESERVE.
Davis PB, Ferkol TW, Ziady A;
WPI; 98-041783/04.
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Key
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusion protein; SC single chain Fv/protamine fusion protein encoding DN exogenous gene; serpin enzyme complex receptor; gene therapy; tarque binding molety; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Delivering compacted exogenous nucleic acid to cells - by the serpin enzyme complex receptor, used in gene therapy Example 9; Pages 120-121; 158pp; English.

This DNA encodes an anti-human SC single chain Fv/protamine
                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; W37085.
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No. 2.
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gene therapy
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26-0CT-1994; 106257.
21-APR-1994; JP-094491.
07-MAR-1994; JP-036065.
(AJIN) AJINOMOTO KK.
Hamura J, Kanayama Y, I
Takeshita T;
WPI; 94-325948/41.
                                                                                                                                                                                                                                                                                                             Q73679 standard; DNA; 729 BP.
Q73679;
Q9-MAY-1995 (first entry)
FV(GP-4) immunosuppressive.
MAb; monoclonal antibody; hybridoma;
FV; antibody variable region; GP-4; F
                                                P-PSDB; R60781.
                                                                                                                                                                                                                                                                                          immunosuppressive;
                       Immunosuppressant polypeptide
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Best Local :
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Q41069 standard; DNA; 848 B
Q41069;
25-AUG-1993 (first entry)
26-10 sFv coding sequence.
Heavy; light; variable; VH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 18; Page 29; 37pp; English.

MAb capable of binding to the gamma chain of the IL-2 receptor, and thus of blocking the IL-2 response, is produced by mouse hybridoma line GP-4 (FERM BP-4640). DNA encoding the variable region of this MAb was expressed in E. coli, yielding FV(GP-4) with immumosuppressive activity.

Sequence 729 BP; 199 A; 169 C; 182 G; 179 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGATAICCTGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGTAAAAGGTGTGCAGCTGCAGGAGTCAGGAGCTGAGGTGGAGGCTGAAGTTCAAT
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                                                                                                                                                                                                                                                   AGCCTACATGGAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG
                                                                                                                                                                                                                                                                                                            TAACTACAACCAGAAGTTCAAGGGCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCAC
                                                                                                                                                                                                                                                                                                                                                                 GCAGAGCCATGGAAAGAACCTTGAGTGGATTGGACTTATTAATCCTTACAATGGTGATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGGGGGTCCAAGCTGGAAATAAAAGGTTCTA---CCTCTGGTTCTGGTAAATCTTCTGA
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                                                                                                                            TGTCTC
                                                                                                                                                    CGTCTC
                                                                                                                                                                                   AGAGAATTACTACGGTAGTAGCTACGGGTTTGCTTACTGGGGCCAAGGGACTCTGGTCAC
                                                                                                                                                                                                                                      AGCCTACATGGAGCTCCACAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG
                                                                                                                                                                                                                                                                                            TAGCTACAACCAGAATTTCAAGGACAAGGCCAGCTTGACTGTAGATAAGTCCTCCAGCAC
                                                                                                                                                                                                                                                                                                                                                   GCAAAGCCATGTAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTTACAATGGTGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                        GAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAA
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                                                                                                                                                                                              -GTTACGGACTGGTACTTCGATGTCTGGGGCGCAGGGACCACGGTCAC
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71.5%;
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Pred. No.
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No. 8e-84;
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(first entry)

VH;

٧L;

region;

antidigitoxin; monoclonal;

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Expression-secretion vectors - for prodn. of biologically active antibody Fv fragments or single chain Fv molecules

Sisclosure; F19 6; 51pp; English.

This sequence encodes a single chain Fv molecule which contains the heavy and light variable portions (VH and VL) of antidigitoxin monoclonal antibody (MAD) 26-10, a signal sequence and a linker between the two variable regions. This sequence was used in the construction of an expression-secretion system for the production of biologically active Fv fragments. The system also contains a DNA sequence encoding the T7 promoter. The secretion expression vector was produced by polymerase chain reaction (see also Q41070-81). Fv fragments comprising only the VH or VL regions, and single chain concleules may be used to specifically bind one or more of the same antigens as the full length antibody from which they are derived.

Sequence 848 BP; 209 A; 216 C; 219 G; 204 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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Synthetic.
Key
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Anthony JG, Ng SC,
WPI; 93-152491/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
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expression-secretion system; T7 promoter; signal peptide; molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-1992;
18-OCT-1991;
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                                                                                                                                                                                                                                                                                                                                                              TCCAACCTKGCTTCTGGAGTCCCTGCTCACTTCAGTGGCGGTGGGTCTGGGACCTCTTAC
                                                                                                                                                                                                                                                                atch 46.6%; cal Similarity 72.9%; 459; Conservative
TTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCATGGAAAGAACCTTGAGTGGATT
                                   CCTGAACTGGTGAAGCCTGGGGCTTCAGTGAGGATGTCCTGCAAGTCTTCTGGATACATA
                                                            CCTGAGGTGGTGAAGCCTGGAGGTTCAATGAAGATATCCTGCAAGACTTCTGGTTACTCA
                                                                                                             GGTTCTGGTAAATCTTCTGAAGGTAAA-----
                                                                                                                                                                                        ACACATGTTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGGGGTGGTTCT
                                                                                                                                                                                                                             AGTCGTAGCCCACCCACGTTCGGAGGGGGGTCCAAGCTGGAAATAAAAGGTTCTACCTCT
                                                                                                                                                                                                                                                                                                     TCTCTCACAGTCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGG
                                                                                                                                                                                                                                                                                                                                          TCCAACCGATTTTCTGGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                   TATTTAAACTGGTACCTGCAGAAGGCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTT 248
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US-777709.
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6. 80
/*tag= h
/note= "P
81. 419
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465 ..821
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420. .464
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/note= "26-10 VH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 331.6; I pred. No. 2.4e. 0; Mismatches
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                                                                                                                                                  -GGTGTGCAGCTGCAGGAGTCAGGA
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                                                                                                                                                                                         Query Match
Best Local Sin
Matches 479;
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28-MAY-1991.
11-JAN-1990; 1
                                                                                                                                                                                                                                                                                                     Disclosure; Fig 3; 26pp; English.

The sequence is an Ndel-HindIII fragment encoding the L and H chains of murine MAD OVB3, joined together via a linker. The sequence is present in clone povB3158-1 in which the 3' end is linked to the 5' end of the coding sequence for PB40, a a Pseudomonas exotoxin lacking domain I. The protein expressed by the clone can be used to kill specific target cells.

Sequence 738 BP; 181 A; 193 C; 192 G; 172 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rapid cloning of antibody genes as single chain immuno-toxins by fusing genes with DNA encoding cytotoxic molecules, to kill target cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q12405;
16-SEP-1991
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P-PSDB; R12798.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     789
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                      CACAATGACTTGCAGGGCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAGAGCC
CACCATGACCTGCAGTGCCATCTCAACTGTAAGTTACATGCACTGGTACCAGCAGAAGTC
                                                                                                                      ATGGACCTGCAGCTGACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTA
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25-APR-1996.
13-OCT-1995; U12840.
13-OCT-1994; US-323445.
(ENZO-) ENZON INC.
Filpula D. Shorr R, Wh
wPI; 96-221949/22.

P--PSDB; R97380.

New antigen binding proteins contg. immunoeffector or cytolytic peptide - attached to variable regions of antibody light or heavy chain, useful in diagnosis and in destroying cancer cells Example 1; Fig 4A-B; 72pp; English.

A novel DNA construct (T29058) codes for a single-chain antigen-binding fusion protein (R97380) comprising the light chain variable region (VL) of monoclonal antibody CC49 linked to the CC49 VH region via a spacer peptide (R97379), with a C-terminal phospholipase A activating protein (PLAP) immunoeffector peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
Key
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Q43291;
27-SEP-1993
                                                          Synthetic.
Key
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Antibody; multivalent;
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Sequence 797 BP; 196 A; 203 C; 195 G; 203
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ding divalent CC49/212 single-chain antigen-binding
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20-NOV-1992; 1
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Sequence
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The number 212 refers to a 14-residue linker. CC49
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25-NOV-1991; US-796936.
(ENZO-) ENZON INC.
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Filpula D, Shorr R,
WPI; 96-221949/22.
P-PSDB; R97381.
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T29059;
03-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antigen binding proteins contg. immunoeffector or cytolytic peptide - attached to variable regions of antibody light or heavy chain, useful in diagnosis and in destroying cancer cells Disclosure; Page 39-40; 72pp; English.

A novel DNA construct (T29059) codes for a single-chain antigen binding fusion protein (R97381) comprising the light chain variable region (VL) of monoclonal antibody CC49 linked to the CC49 VH region via a spacer peptide (R97379) and with an N-terminal phospholipase A activating protein (PLAP) immunoeffector peptide (R97368). It can be used to produce the fusion protein in transformed host cells. The fusion protein combines the tumour antigen-binding capability of CC49 with the immunoeffector function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLAP CC49/212 SCA DNA construct.
Single chain antigen-binding tasion protein;
cytostatic; phospholipase A activating prote;
therapy; monoclonal antibody; CC49; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigen-binding capability of PLAP.
Sequence 803 BP; 198 A
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13-OCT-1995; U12840.
13-OCT-1994; US-323445
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ORGANISM

Unknown.

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PAT 07-JAN-1997

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Expression

Incation Combinations thereof, and therapeutic and diagnostic uses thereof

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Local Similarity 100.0%; hes 720; Conservative

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King, C.R.Cohter, Kasprzyk, P.G. and Bir

Anti-erbbs-2 antibodies, combinations
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Patent: US 5587458-A 1 24-DEC-1996;
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                                                                                                               Mus sp.
Eukaryotae;
Vertebrata;
                                                                                                                                                                      Synthetic
S39590
g251113
                                                      1 (bases 1 to 711)
Batra,J.K., Kasprzyk,P.G., Bird,R.E., Pastan,I. and King,C.
Recombinant anti-erbB2 immunotoxins containing Pseudomonas
Proc. Natl. Acad. Sci. U.S.A. 89 (13), 5867-5871 (1992)
                                                                                                    Mus.
GenBank staff at the National Library of Medicine entry [NCBI glibsq 108547] from the original journ This sequence comes from Fig. 1.
Location/Qualifiers
                                               92335198
                                                                                                                                                 Mus
                                                                                                                                                                                                          anti-erbB2
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imnmunotoxin antigen
Recombinant Partial, 7
                                                                                                              mitochondrial eukaryotes; Metazoa;
Eutheria; Rodentia; Sciurognathi; N
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Pred. No. 3.4e
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ismatches 131;
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711 nt].
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                       journal
                                                                                                                Muridae;
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[mice, Other
                                                                                                                           Chordata;
                      created this nal article.
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                                                                               TCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGC
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                                                                                                     TCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGC 644
                                                                                                                                                                                  AGGGCCTGGAATGGATTGGATGGATTCATCCTGAGAATGGTAATACTGTATATGACCCGA
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/gene="anti-erbB2 imnn
/note="This sequence c
/codon_start=1
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/translation="MDLOLTQSPAILSASPGEKVTMTCRATPSVSYMHWYQQKPGSSPKPHTVTSNLASGVPARESGGGSGTSYSLTVSRVEAEDDATYYCQQWSRSPPTEGGGSKENETYTTSNLASGVPARESGGGSGTSYSLTVSRVEAEDDATYYCQQWSRSPPTEGGGSKLEIKGSTSGSGKSSEGKGVQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSKLEIKGSTSGSGKSSEGKGVQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSKHGKNIFTVDKSSSTAYMELLSLTSEDSAVYYCARRVTDWYFGTYVS"

182 c 190 g 164 t
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/db_xref="taxon:10095"
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/gene="anti-erbB2 imnmunotoxin
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79.6%;
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Pred. No. 3.4e-123;
0; Mismatches 131;
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US 5582826
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FEATURES
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AUTHORS
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SOURCE
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                                                                                    TACGATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACACCATCCTCCAGCACAGCC
                                                                                                                                                      TATGACCCGAAATTCCAGGGCAAGGCCAGTATAACAGCAGACACATCCTCCAACGCGGCC
                                                                                                                                                                                                          AGGCCTGAACAGGGCCTGGAATGGATTGGATGGATTCATCCTGAGAATGGTAATACTGTA
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                                      AGCCGGAACTGGGTCTACTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTC
                                                            TACTACTATAGTGCTTACTATGCTATGTACTACTGGGGTCAAGGAACCTCGGTCACCGTC
                                                                                                                                                                                          AGGCATGGACAAGGCCTTGAGTGGATTGGAAATATTTATCCTGGTAGTGGTAGTACTAAC
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g1821826
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Patent: US 5582826-A 1 10-DEC-1996;
Location/Qualifiers
1. 732
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Shimamura, T., Hamuro, J., Nak
Takeshita, T.
Monocional antibodies which
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57; Conservative
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204 c 182 g
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76.7%;
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Pred. No. 9.3e-123;
0; Mismatches 160;
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Patent number JP 1995313188-A/1,
AJINOMOTO CO INC, SUGAMURA KAZUO,
                                                                                                                                                                                                                                                                                                                                                                                                                              08-OCT-1997
08-OCT-1997
                                                                                                                                             cDNA encoding a receptor gamma
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SUGAMURA KAZUO, TAKESHITA TOSHIICHI
C12P21/08,A61X39/395,A61X39/395,C12N1/21,C12N5/20,
C12N15/13//C12N15/06,
(C12P21/08,C12R1:19),(C12P21/08,C12R1:91),(C12N1/21,C12R1:19);
                          Mus sp. (mouse)
JP 1995313188-A/1
05-DEC-1995
21-APR-1994 JP 1994082836
21-APR-1993 JP 93P 94491, 07-MP
SHIMAMURA TOSHIAKI, HAMURO JUNJI,
        ACCTGCAGTGCCAGCTCAAGTGTA-----AGTAACATGCACTGGTATCAGCAGAAGTCA 114
ACCTGCACTGCCAGCTCAAGTGTAAGTTCCAGTTACTTGCACTGGTACCAGCAGAAGCCA
                                                                                                                                                   mat_peptide
                                                                                                                                                                                                            strandedness:
                                                                                                                                                                                                    topology: Linear;
                                                       al Similarity
557; Conser
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                                                                                                                                                                                                                                                                                                                                                              Metazoa; Ch
hi; Muridae;
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                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                a monoclonal
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                                                                                           180
                                                                                                         /organism="Mus
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52,
                                                                                                                                                                                                            Double;
                                                                                                                                                                                                                                                                                                                                                              Chordata; Vertebrata; ae; Murinae; Mus.
                                                                                                                                          /organism-"Mus sp."
/cell_type-"hybridoma"
/cell_line-"GP-2"
1. 732
/product="anti-IL-2 rec
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                                                               60.0%;
76.7%;
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                                                       0;
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REFERENCE
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Synthetic
                                                                                                                                                           artificial sequence.

1 (bases 1 to 738)
Chaudhary, V.K., Batra, J.K., Gallo, M.G., Willingham, M. Fitzgerald, D.J. and Pastan, I.
A rapid method of cloning functional variable-region in Escherichia coli as single-chain immunotoxins Proc. Natl. Acad. Sci. U.S.A. 87, 1066-1070 (1990)
                                                                                                                                                                                                                                                                 Mouse hybridoma, cDNA artificial sequence
                                                                       /organism="artificial
/db_xref="taxon:29278"
<1. .>738
/transl_table=11
/db_xref="PID:9207975"
/translation="HMENVLTQSPAIMSASPGEKVTMTCSAISTVSYMHWYQQKSSTS
                                         /note-"OVB3 I
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GPX7.
E13599
93252401
JP 1997220092-A/2.
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TKLELKEGKSGGSGSKVDDVQLVESGGGLVQPGGSRQLSCAASGFTFSSFGMHWVR
QAPEKGLEWVAYISRGGNTIYYANTVKGRFTISRDNPKNTLFLQMTSLRSDDTAMYYC
ARSHYYCYFYAMDYWGGCTTLTVSSKAF*
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E KAdda,T., Yasukawa,K., Imanaka,T. and Takagi,M...

FRODUCTION OF SINGLE-STRAND FV ANTIBODY
Patent: JP 1997220092-A 2 26-AUG-1997;

TOSOH CORP
OS None
OC Artificial sequences.
PN JP 1997220092-A/2
PD 26-AUG-1997
PF 15-FEB-1996 JP 1996027622
PI EKIDA TEIJI, YASUKAWA KIYOSHI, IMANAKA TADAYU
MASAHIRO
PC C12N15/09,C12N1/21,C12P21/08,(C12N1/21,C12R1:P);
CC C12R1:19);
CC strandedness: Double;
CC topology: Lineat;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FH Key Location/Qualifiers
FT source /organism-'Antificial sequence
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/db_xref="taxon:32644"
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IgG3.
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Z95478 AF004405
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/note="recombinant gene"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAATCTTCTGAAGGTAAAGGTGTGCAGCTGCAGCAGTCTGGGGTTGAGCTTGTCCGAGGA 396
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                                                                                                                                                                                                                                                                                                                                                                              Mus musculus 1
Z95477 AFOC
                                                                             2 (bases 1 to 822)
Schouten,A., Roosien,J., de Boer,J.M., Wilmink,A., Ross Bosch,D., Stiekema,W.J., Gommers,F.J., Bakker,J. and Sc Improving scFv antibody expression levels in the plant FEBS Lett. 415 (2), 235-241 (1997)
                                                                                                                                                                                      Direct Submission
Submitted (07-MAY-1997) Dept.
Agricultural University, P.O.
                                                                      98010486
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1 (bases 1 to 822)
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Julus mRNA fc
7 AF004404
/organism="Mus musculus"
/note="recombinant gene"
                                                Location/Qualifiers
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x 8123, Wageningen 6700
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                                                                                                                                       Rosso, M.N.,
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                                                            CTATGACTGCAGACACATCCTCCAACACACGCCTACCAGCAGCCTCAGCAGCCTGACATCTG
                                                                                                                                     GATGGATTCATCCTGAGAATGGTAATACTGTATATGACCCGAAATTCCAGGGCAAGGCCA 559
                                                                                                                                                                                                   TTAAAGACTATTATATCCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAATGGATTG
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                                                                                           GATGGATTGATCCTAAGAATGGTGATACTGATTATGCCCCGAAGTTCCAGGGCAAGGCCA
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 AGGACACTGCCGTCTATTACTGTAGTGCCTATGGTGACTTCGACGCCTAC
                             AGGACACTGCCGTCTATTACTGCTGCTTCTTATTACTACTATAGTGCTTAC
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436; Conser
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coding sequence"
769. 801
/note="0-myc tag coding sequence"
808. 819
/note="NDEL coding sequence"
a 203 c 221 g 184 t
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/translation="MDVVMTOTPLSLFVSLGDQASISCRSSQTILHSNGNTYLEWFLQ
KPGQSPKLLIKVSNRESGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPY
TFGGGTKLEIKGGSGGGGGGGGGGGSEVQLQQSGAELVRSGASVKLSCTASDFNI
KDYYIHWVKQRPEQGLEWIGWIDPKNGDTDYAPKFQGKATMTADTSSNTAYLQLSSLT
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/note="Linker peptide coding sequence"
394. .741
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742. .756
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/product="IGG1/kappa antibody"
/db_xref="PID:el167935"
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73.9%;
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Pred. No. 1.5e-90;
0; Mismatches 139;
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Matches 491; Conserv
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 TTGTCCTGCAAAGCTTCTGACTTCAACATTAAAGACTATTATATCCACTGGGTGAAGCAG
                         TCCGAGGTCAAGCTGCAGGAGTCTGGGGGGAGGCTTAGTGAAGCTTGGCGGGTCCCTGAAA
                                                     ---GGTGTGCAGCTGCAGCAGTCTGGGGGTTGAGCTTGTCCGAGGAGGGGGCCTTAGTCAAG 411
                                                                               GGGACAAAGTTGGAAATAAAAGGTTCTACCTCCGGATCTGGTAAATCTTCTGAAGGTAAA
                                                                                                                                    GAAGATGTTGCCACTTACTACTGCCAGCAGGGTAGTAGTATACCGCTCACGTTCGGTGCT
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OC THE PN JP 11
PD 26-A
PD 26-A
PD EKID
PI EKID
PI EKID
PC C12N
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PC C12N
PC C12R
CC Stra
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TOSOH CO
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Ekida, T., Yasukawa, K., Imanaka, T. and Takagi, M.
ERODUCTION OF SINGLE-STRAND FV ANTIBODY
Patent: JP 1997220092-A 1 26-AUG-1997;
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JP 1997220092-A/1.
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DNA encoding a single chain Fv antibody of anti-T3 antibody
E13598
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Artificial sequences.
JP 1997220092-A/1
26-AUG-1997
15-FEB-1996 JP 1996027622
EKIDA TEIJI, YASUKAWA KIYOSHI, I
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hypothetical: No;
anti-sense: No;
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192 c 197 g
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Matches 504; Conservative
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                                                                                                                    GCTCACCCAGTCTCGAGCAATCATGTCTGCATCTCCAGGGGAAAAGGTCACCATGACCTG
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Sequence
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Ladner, R.C. and Bird, R.E.
SINGLE POLYPEPFIDE CHAIN BINDING MOL
Patent: WO 8801649-A 10 10-MAR-1988;
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Pred. No. 1.4e-88;
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          TGCTGCCACTTATTGTTATCAGGGGAGTGGGTACCCATTCACGTTCGGCTCGGGGAC 299
                                                                                                   CTCCCCCAAACTCTGGGTTTATGACACATCCAAACTGGCTTCTGGAGTCCCAGGTCGCTT 179
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TGCTGCCACTTATTACTGCCAGCAGTACAGTGGTTACCCACTCACGTTCGGTGCTGGGAC
                                           CAGTGGCAGTGGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGTGTGGAGGCTGAAGA
                                                                                       CTCCCCCAAACTCTGGATTTATAGCACATCCAACTTGGCTTCTGGAGTCCCTGCTCGCTT 191
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108679
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Ladner,R.C. and Bird,R.E.
SINGLE POLYDEPTIDE CHAIN BINDING MOI
Patent: WO 8801649-A 12 10-MAR-1988,
Location/Qualifiers
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Pred. No. 1.3e-85;
0; Mismatches 208;
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Best Local Similarity
Matches 472; Conser
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                         ACCTCCCCAAACTCTGGGTTTATGACACATCCAAACTGGCTTCTGGAGTCCCAGGTCGC
                                                                    ACCTGCAGTGCCAGCTCAAGTGTA---AGTAACATGCACTGGTATCAGCAGGAAGTCAAGC 117
                                                                                              ATTCTGCTGACACAGTCTCCAGCCTCCTATCTGCATCTGTGGGAGAAACTGTCACCATC
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Sequence 3
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Patent: US 5582826-A 3
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Pred. No. 1e-81;
0; Mismatches 2
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                                                            Takeshita T.;
"IMMUNOSUPPRESSIVE AGENT";
Patent number JP 199531318
                                                                                                                                   Mus sp.
Eukaryota; Metazoa; Chordata; Vertebrata;
Sciurognathi; Muridae; Murinae; Mus.
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Mus sp. (mouse)
JP 1995313188-A/2
05-DEC-1995
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                                                                                           GACCCGAAATTCCAGGGCAAGGCCAGTATAACAGCAGACACATCCTCCAACGCGGCCTAC
                                                                                                                  CATGTAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTTACAATGGTGCTACTAGCTAC
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(C12P21/08,C12R1:19),(C12P21/08,C12R1:91),(C12N1/21,C12R1:19);
Key Location/Qualifiers
                                             CTTCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGCTTCTTATTAC
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/organism="Mus
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/cell_type="hybridoma"
/cell_line="GP-4"
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Pred. No. le-81;
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Artificial gene cDNA t artificial sequence artificial sequence.

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Synthetic single-chain Fv fusion protein (DA4.4, constructed from variable light and heavy chain monoclonal antibody DA4.4, 3' end of cds.
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Nagle,J.W. and Filpula,D.
Production of engineered
Escherichia coli
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90; Conservative
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/transl_table=11
/function="binds human IgM"
/function="binds human IgM"
/product="binds human IgM"
/product="binds human IgM"
/product="fision protein"
/db_xref="pin:g310740"
/translation="DVWMTQSSSSLAMSVGQKVTMSCKSSQSLLNSSNQKNYLAWYQQ
KPGQSPELLVYEASTRESGVPDRFIGSGSGTDFTLTISSVQAEDLADYFCQQHYSTPF
TFGSGTKLEIKGSTSGSGKSSEGKGQVQLQQPGAEFVKPGAPVKLSCKASGYPFTTYW
VNMMKQREGRGLEWIGRIDFYDSETLYNQKFKDKATLTVDKSSSTAXIQLSSLTSEDS
AVYYCARETYDYPFAYWGQGTLVTVS"
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/db_xref="taxon:29278"
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Pred. No. 3.2e-81;
0; Mismatches 216;
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COMME	TITLE JOURNAL	REFERENCE AUTHORS	NID KEYWORDS SOURCE ORGANISM	RESULT 1 AA691311 LOCUS DEFINITION ACCESSION
Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP	Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R. The WashU-HHMI Mouse EST Project Unpublished (1996)	Eukaryotae; wetazoa; Chordata; Vertebrata; Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 396) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,	g2692247 EST house mouse. Mus musculus	AA691311 396 bp mRNA EST 16-DEC-1997 vsl4f01.rl Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone 1138201 5' similar to 9b:X67211 M.musculus rearranged immunoglobulin kappa light chain (MOUSE);, mRNA sequence. AA691311

ALIGNMENTS

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                                                                                                                                                                          AA592800 344 bp mRNA EST 17-SEP-1997 vo25g11.rl Barstead mouse irradiated colon MPLRB7 Mus musculus clone 1050980 5' similar to gb:X67211 M.musculus rearranged immunoglobulin kappa light chain (MOUSE);, mRNA sequence.
AA592800
Eukaryotae: Metazoa; Chordata; Vertebrata; Mammalia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 344)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morr Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Mc
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This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
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                                                                                                          Mus musculus
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(db_xref="taxon:10090"
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/clone_lib="Barstead mouse irradiated
/dev_stage="8 weeks"
/lab_host="DH10B"
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LOCUS

DEFINITION AI180569

AI180569 310 bp mRNA EST 08-OCT-1998 uc70f09.rl Soares mouse mammary gland NbMMG Mus musculus cDNA clone 1431017 5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); gb:M12376 Mouse immunoglobulin H-chain V-region pseudogene

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Location/Qualifiers
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This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further 1
MGI:582556
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Tel: 314 286 1800
Fax: 314 286 1810
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                                    CCGAAATTCCAGGGCAAGGCCAGTATAACAGCAGACACATCCTCCAACGCGGCCTACCTT 597
                                                                                                 GAACAGGGCCTGGAATGGATTGGATGGATTCATCCTGAGAATGGTAATACTGTATATGAC
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AI180569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4444 Forest Park Parkway, Box 8501,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 310)
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RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Site_2: Eco RI; 1st strand cDNA was primed with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="1431017"
/clone_lib="Soares mouse
                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
77 c 85 g 67 t
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: Robert_Strausberg@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="adult"
/lab_host="DH10B"
132 c 106 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NCI_CGAP_Pr28"
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Pred. No. 1.8e-35;
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GGGCAAGGGCTTGAGTGGGTGGGAATGATCAATTCTAGTGATGGTTATATAAGTAACGCA
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Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 284.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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AA569186
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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1 (bases 1 to 387)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Vector: pampl0; mRNA made from liposarcoma, cDNA made by oligo-dT priming. Non- directionally cloned. Size-selected on agarose gel, average insert size 600 l Reference: Krizman et al. (1996) Cancer Research
                                                                                                                                                                                                                                                                                                                                                                          <u>^</u>
                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:1061683"
/clone_lib="NCI_CGAP_Lip2"
/tissue_type="liposarcoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref-"taxon:9606"
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Matches 205;
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The WashU-HHMI Mouse EST Project Unpublished (1996)
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1 (bases 1 to 294)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Moorte,B., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
MGI:896378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4444 Forest Park Parkway,
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                                                                                                                                                                                                  /clone="1363158"
/clone_lib="Soares 2NbMT"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                            /lab_host="DH10B"
68 c 77 ;
                                                                                                                                                              /tissue_type="Thymus"
                                                                                                                                                                                   /sex="male"
                                                                                                                                           dev_stage="4 weeks"
Score 133.8; DB 28
Pred. No. 1.2e-31;
0; Mismatches 82;
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zw27f11.rl Soares ovary
5' similar to gb:X06764
                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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AA456778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
WashurMerck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
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/db_xref="taxon:9606"
/clone="770541"
                                          /clone_lib="Soares ovary
                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
    /tissue_type="ovarian tumor"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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M., Martin,J.,
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                                                     Addams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gooayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S.,
Kelley, J.M., Klinek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,
Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T.,
Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,
Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,
Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A.,
Coleman, T.A., Collins, E.-J., Dinke, D., Feng, P., Ferrie, A.,
Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H.,
Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,
Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A.,
Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of CDNA Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGGACAAAGTTGGAAATAAAAGGTTCT 321
Unpublished (1995)
Other_ESTs: THC24356
Contact: Venter, JC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T27593 393 bp mRNA EST 06-SEP-1995 EST100653 Homo sapiens cDNA 5' end similar to immunoglobulin light chain, V region (GB:L01279) (HT:3043).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deuterostomia; Chordata; Vertebrata; Gnathostomata; Os
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 393)
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241 AGGTTCAGTGGCAGTGGGTCTGAGACAGÄCTTCACTCTCAACATCGGCAAGACTGGAGCC
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                                                                                                                   CGCTTCAGTGGCAGTGGGTCTGGAAACTCTTACTCTCTCACGATCAGC-AGCATGGAGGC 233
                                                                                                                                                                                                                                                                                                           ACCTGCAGTGCCAGCTCAAGTGTAAGTAACA-----TGCACTGGTATCAGCAGAAGTCA 114
                                           TGAAGATGCTGCCACTTATTATTGTTATCAGGGGAGTGGGTACCCATTCACGTTCGGCTC
                                                                                                                                                                                     GGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCAACTGGCATCCCAGAC
                                                                                                                                                                                                                  AGCACCTCCCCAAACTCTGGGTTTATGACACATCCAAACTGGCTTCTGGAGTCCCAGGT
                                                                                                                                                                                                                                                                                                                                                                          ATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTC 120
TGACGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTCGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B (ampicillin resistant)" <1. .>400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 122.8;
Pred. No. 3.
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BASE COUNT
ORIGIN
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AA295311
LOCUS
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Best Local (
                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
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Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
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Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACAAAGTTGGAAATAAAAGGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCTGCAGTGCCAGCTCAAGTGTAAGTAACATGC---ACTGGTATCAGCAGAAGTCAAGC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGTTGCAACTTACTACTGTCAACAGAGTTNCACTTATGNCTCGGACGGTTGGCCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATGCTGCCACTTATTATTGTTATCAGGGGAGTGGGTA-CCCATTCACGTTCGGCTCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCAGTGGCAGTGGGTCTGGAAACTCTTACTCTCACGATCAGCAGCAGCATGGAGGCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCTCCCCAAACTCTGGGTTTATGACACATCCAAACTGGCTTCTGGAGTCCCAGGTCGC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCCTC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACCAAGGTGGAGGTCAAACGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCAGTGGCTCTGGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAGCCCCTAAGCTCCTGATCTCTGCTGCATCCAATTTGCGAAGTGGGGTCCCATCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTTGCCGGGCAAGTCAGAGCATTAGCACCTTTTTAAATTGGTATCAGCAGAAACCAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST100471 Pancreas immunoglobulin kapp AA295311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org).
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryotae; 1
                                                                                                                                                                                                                                                                                                                                                           Vertebrata; Mammalia;
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Clopper Rd,
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k: 3018699423
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<1. .>393
1 113 c 96 g 9
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d, Gaithersburg, MD 20878
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pa light chain, VJ regions, mF
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Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGCAGCTGACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAAAAAGGTCACCATG 60
                                                                                                                                                                                                                                                                                    GATTTTNCAGTTTATTACTGTCAGCAGTATAATAACTGGGCATTCA
                                                                                                                                                                                                                                                                                                                   GATGCTGCCACTTATTGTTATCAGGGGAGTGGGTACCCATTCA 283
                                                                                                                                                                                                                                                                                                                                                                                   TTCAGTGGCAGTGGGGTCTGGAAACTCTTACTCTCTCACGATCAGCAGCATGGAGGCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                    CAGGCTCCCAGGCTCCTCATCTATGGTGCATCCATCAGGGNCACTGGCATCCCAGCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATAGTGATGACGCAGNTTNCAGCCACCCTGTCTGTGTNTCCAGGGGAAAGAGCCACCCTN 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Raymond, L., Wei, Y.E., Man, Rosen, C.A., Haseltine, M.C., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, M.C., Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                 AA710291 345 bp mRNA LST LATTON AA710291 345 bp mRNA vt53a04.rl Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone 1166766 5' similar to 95:X02464_rnal IG KAPPA CHAIN PRECURSOR V-IV REGION (HUMAN); gb:J00560 mouse 19 kappa mrna from mopc21 6 other myeloma mrna 3' (MOUSE); mRNA sequence.
                                                                                                AA710291
g2720209
Mus musculus
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 345)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: arkerlav@tigr.org
For clone availability, additional sequence ar
information related to this EST, please check
Index (http://www.tigr.org/tdb/hg1/hg1.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 3018699423
                                                              house mouse
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ECORI; Site_2: XhoI"
/db_xref-"ATCC (inhost):190766"
/db_xref-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Pancreas tumor
/dev_stage="adult"
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Pred. No. 5.4e-27;
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                                                          299 CAAAGTTGGAAATAAAA 315
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                                                                                                                                                                                                                                                                                                                                                                                                 ATTGTGATGACCCAGTCTCAAAAATTCATGTCCACATCAGCTGGAGACAGGGTCAGCGTC 87
                                                                                                                    ATGCTGCCACTTATTATTGTTATCAGGGGAGTGGGTACCCATTCACGTTCGGCTCGGGGA 298
                                                                                                                                                                                             TCAGTGGCAGTGGGTCTGGAAACTCTTACTCTCTCACGATCAGCAGCATGGAGGCTGAAG
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                                                                                                                                                                                                                                                                                                                       ACCTGCAAGCCAGTCAGAATGTGGGTACTAATGTAGCCTGGTATCAAGAGAAACCAGGGC 147
                                                                                                                                                                                                                                                                                                                                                            ACCTGCAGTGCCAGCTCAAGT--GTAAGTAACATGCACTGGTATCAGCAGAAGTCAAGCA 118
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                                                                                                                                                                        TCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATGTGCAGTCTGAAG
                         CCAAGCTGGAAATAAAA 344
                                                                                                ACTTGGCAGAGTATTTCTGTCAGCAATATAACAGCTTTCCGTACACGTTCGGAGGGGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
WashIngton University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
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The WashU-HHMI Mouse EST Project
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h quality sequence stop: 140.
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="FVB/N"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; Tissue obtained from 8 week old mouse. Colon was harvested 72 hours afte irradiation with 1400 Gys. 1st strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adaptors [AATTCGGATCCTTG], digested with Not I and clain to the Not I and Eco RI sites of the modified pT7T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Barstead mouse irradiated colon MPLRB7"
/dev_stage="8 weeks"
/lab_host="DH10B"
81 c 88 g 81 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vector. Library constructed by /db_xref="taxon:10090" /clone="1166766"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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Pred. No. 5.
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AUTHORS
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ORGANISM
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102 GCCTGGTATCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCGTCCAGG 161
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                                                                                                                      --CTGGTATCAGCAGAAGTCAAGCACCTCCCCAAACTCTGGGTTTATGACACACATCCAAA 153
                                                                                        CCAGGGGAAAGAGCCGCCCTCTCCTGCAGGGCCAGTCAGCGTGTTAGCAGCAGTCACTTA 101
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human
Homo sapiens
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AA345486
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Seq primer: M13 Reverse.
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Kerlavage, AR
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3018699423
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/note="Organ: gall bladder; Vector:
Site_1: EcoRI; Site_2: XhoI"
/db_xrof="ATCC (inhost):147008"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                113
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                                                                                                                                                                                    Score 118.8; DB
Pred. No. 6.7e-27
D; Mismatches 9
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                                                                                                                                                                                                                                                                                                                                     Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Kerlavage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96026280
Other_ESTs: THC168243
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Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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Seq primer: M13 Reverse.
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        85
/db_xref="ATCC (inhost):190705"
/db_xref="taxon:9606"
/clone_lib="Pancreas tumor I"
/dev_stage="adult"
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a 107 c 94 g 77 t
                                                                                                                                                      /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
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Matches 178; Conserv
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Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human
                                                                                                                                    The Institute for Genomic Research 9712 Medical Center Drive, Rockville,
                                                                                                                                                                                             Bioinformatics
                                                                                                                                                                                                                Contact: Kerlavage, AR
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                                                                                                                                                                                                                                                                                              Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Ho
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Pred. No. 1.5e-26;
0; Mismatches 85;
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162; Conserv
                                                                                                                                                                                                                    1 (bases 1 to 379)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
Washdy-Merck EST project
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA291381 379 bp mRNA EST
zt44g02.rl Soares ovary tumor NbHOT Homo sapiens
5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR
                                                                                                                                                   Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
g1939359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                 Homo
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
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Ecorl; Site_2: Xhol"
/db_xref="ATCC (inhost):192041"
/db_xref="taxon:9606"
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<1. .>333
85 c 80 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                             ng69c07.sl NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940044 similar to gb:M63438 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN); mRNA sequence.
                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/nclogap.
National Cancer Institute, Cancer Genome Anat
Tumor Gene Index
                           Emmert-Buck, M.D., Ph.D.
                                                                                                                   Unpublished (1997)
                                                                                                                                                                                                                                      Homo sapiens
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                                                           Email:
                                                                                      Contact: Robert Strausberg,
                                                                                                                                                                                                                       Eukaryotae;
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                                                                                                                                                                                                            Vertebrata;
cDNA Library Preparation: David B. Krizman, cDNA Library Arrayed by: Greg Lennon, Ph.D.
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                                                                         (301) 496-1550
                                                          Robert_Strausberg@nih.gov
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/lab_host="DH108 (ampicillin
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/clone="725234"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares ovary tumor
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Pred. No. 3.2e-26;
                                           Jeffrey Medeiros,
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                                                                                      GGGACCAAGGTGGAAATCAAACGAACT 411
                                                                                                        GGGACAAAGTTGGAAATAAAAGGTTCT 321
                                                                                                                                               GAAGATTCTGCAGTTTACTATTGTCAGCACTATGGTACCTCATTATGGACATTCGGCCAG
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High quality sequence stop: 413.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="IMAGE:940044"
/clone=11b="NCI_CGAP_Lip2"
/tissue_type="11posarcoma"
/lab_host="DH10B"
<1...>418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/note="Vector: pAMP10; mRNA made from liposarcoma, cDNA
/made by oligo-dT priming. Non-directionally cloned.
Size-selected on agarose gel, average insert size 600 bp.
Reference: Krizman et al. (1996) Cancer Research
56:5380-5383."
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127 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.0%; Score 115.4; DB 21; 63.9%; Pred. No. 7.8e-26; tive 0; Mismatches 111;
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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OM nucleic nucleic search, using sw model

Run

Мау 13, 1999, 09:55:24 ; Search time 59.56 Seconds
(without alignments)
2274.252 Million cell updates/sec

Title: Perfect score: US-08-704-178-2 720

Sequence: 1 ATGCAGCTGACCCAGTCTCC......CGGTCACCGTCTCCTCATAA 720

Scoring table: IDENTITY_NUC

Searched: 240622 seqs, 94065609 residues

N_Geneseq_34:*

Database :

Pred. No. score grea and is der No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

SUMMARIES

4444098765433	Result No.
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TCCCCCAAACTCTGGGTTTATGACACATCCAAACTGGCTTCTGGAGTCCCAGGTCGCTTC 180

ACCTGCAGTGCCAGCTCAAGTGTAAGTAACATGCACTGGTATCAGCAGGAAGTCAAGCACC 120

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CAGCTGCAGCAGTCTGGGGTTGAGCTTGTCCGAGGAGGGGCCTTAGTCAAGTTGTCCTGC 420

AAGTTGGAAATAAAAGGTTCTACCTCCGGATCTGGTAAATCTTCTGAAGGTAAAGGTGTG AAGTTGGAAATAAAAGGTTCTACCTCCGGATCTGGTAAATCTTCTGAAGGTAAAGGTGTG GCTGCCACTTATTATTGTTATCAGGGGAGTGGGTACCCATTCACGTTCGGCTCGGGGACA GCTGCCACTTATTGTTATCAGGGGAGTGGGTACCCATTCACGTTCGGCTCGGGGACA

360 360

CAGCTGCAGCAGTCTGGGGGTTGAGCTTGTCCGAGGAGGGGGCCTTAGTCAAGTTGTCCTGC

420

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Query Match
Best Local Similarity
Matches 720; Conserv

100.0%; ilarity 100.0%; Conservative 0;

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Score 720; DB 1; Pred. No. 2e-182; Mismatches 0;

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regressed after it days.) Sequence 720 BP; 184 A; 178 C; 179 G; 179 T;	animals g	growing tumours	domain of gp185 erbB-2. Nude mice manipulated to produce rapidly			2 23 and 21 (Q55180/R45442; Q55181/R45443) is a NIH/3T3 cell			Ī	2 monoclonal antibodies which recognise different								0 06-JAN-1994.	WO9400136-A.		_			monoclonal antibody; ss.			21-JUL-1994 (first entry)	Q55181;	0	Q55181	RESOLT		ALIGNMENTS	

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 g
                                                                                                                 PT Single chain antibodies specific for erbB-2 protein, gp185 - with pT labels or cytotoxin, useful for detection and treatment of tumour PT cells expressing this protein
PS Example 9; Columns 27-30; 28pp; English.

CC The present cDNA sequence codes for a claimed single-chain antibody, e21
CC designated e21(FV), which binds to erbB-2. Monoclonal antibody e21
CC was generated by immunising mice with N/erbB-2 cells overexpressing CC was generated by immunising mice with N/erbB-2 cells overexpressing CC the gp185 protein, removing spleen cells and producing hybridomas CC by standard techniques. Messenger RNA coding for the anti-erbB-2 CC monoclonal antibody was isolated and converted to cDNA. Regions CC coding for the heavy- and light- chain variable regions were then CC linker. The resulting single-chain antibody is useful for in vitro CC diagnosis of tumour cells which overexpress the erbB-2 gp185 cC marker, e.g. breast, overlan and non-small cell lung carcinomas, CC and, when coupled to a cytotoxic agent, to treat such tumours.

SQ Sequence 720 BP; 184 A; 178 C; 179 G; 179 T;
                                                     Query Ma
Best Loc
Matches
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07-CCT-1991; 772270.

07-CCT-1991; US-772270.

30-JUN-1992; US-906555.

14-MAY-1993; US-961092.

(ARON-) ARONEX PHARM INC.

Bird RE, Kasprzyk PG, Ki

WPI; 97-064831/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-1997 (first entry)
05-JUN-1997 (first entry)
Single-chain anti-erbB2 antibody e21(Fv) cDNA.
Single chain antibody; variable region; light chain; heavy chain; Single chain antibody; variable region; light chain; heavy chain; breast cancer; ovarian cancer; non-small cell lung carcinoma; breast cancer; ovarian cancer; non-small cell lung carcinoma;
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ches 720; Conserv
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II T17728

ID T17728

AC T17728;

AC T17728;

AC T17728;

DE Anti-erbB2 scFv cDNA,

T1778;

DE Anti-erbB2 scFv cDNA.

Concoprotein; erbB2; cell proliferation; tumour; cancer;

KW intracellular antibody homologue; single chain antibody; scFv;

KW gene therapy; ds.

S Synthetic.

PN W09607321-A1.

PD 14-MAR-1996.

PP 23-AuG-1995; US-401339.

PR 06-SEP-1994; US-301339.

PR 06-JUN-1995; US-468252.

PR 06-JUN-1995; US-468252.

PR (UABR-) UAB RES FOUND.

PI Curiel DT, Deshane J;

PR (P-SDB; R94020./17.

PR P-PSDB; R94020./17.

PR P-PSDB; R94020.

PT Inhibition of proliferation or survival of, esp. malignant erbB2, protein intracellularly

PS calim 42; Page 29-30; 48pp; English.

CC (R94019) linked to a second sequence encoding a signal peptide chain Fv fragment (R94020) that binds a human erbB2 oncoprotein.

CC The anti-erbB2 sFv portion is obtained by PCR using e23scFv
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RESULT
T65006
ID T0
AC T1
AC T1
AC T1
AC T1
ODT 0:
KW 5:
KW 6:
KW 6:
KW 6:
KW 7:
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endoplasmic reticulum.
plasmid or viral vecto
                                                                                                                            05-JUN-1997 (first ent
Single-chain anti-erbB2
Single chain antibody;
breast cancer; ovarian
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Sequence 711
                                                               Synthetic.
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                      mat_peptide
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nilarity 79.6%;
Conservative
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/*tag=
                                      Location/Qualifiers
                                                                                               i-erbB2 antibody e23(Fv) cDNA.
ibody; variable region; light chain; heavy
varian cancer; non-small cell lung carcinon
treatment; cytotoxic agent; erbB-2; ds.
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erbB-2; ds.
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Example 8; Columns 25-8; 28pp; English.

Example 8; Columns 25-8; 28pp; English.

The present cDNA sequence codes for a claimed single-chain antibody, classing the protein protein
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Best Local Similarity
Matches 511; Conserv
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24-DEC-1996.
07-OCT-1991; 772270.
07-OCT-1991; US-772270.
30-JUN-1992; US-906555.
14-MAY-1993; US-061092.
(ARON-) ARONEX PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bird RE, Kasprzyk PG, King
WPI; 97-064831/06.
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                                                                                                                                                                                                                                                                                                                                                               AGTTGGAAATAAAAGGTTCTACCTCCGGATCTGGTAAATCTTCTGAAGGTAAAGGTGTGC
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AGTTCAAGGGCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCACAGCCTACATGGAGC
                      AATTCCAGGGCAAGGCCAGTATAACAGCAGACACCTCCAACGCGGCCTACCTTCAGC
                                                                                                       AGGGCCTGGAATGGATTGGATGCATTCATCCTGAGAATGGTAATACTGTATATGACCCGA
                                                                                                                                                                     AGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCATGGAA
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79.5%;
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Pred. No. 2.8e-106;
L; Mismatches 131;
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Best Loc
Matches
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21-APR-1993; JP-094491.
07-MAR-1994; JP-036065.
(AJIN) AJINOMOTO KK.
Hamura J, Kanayama Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q73678 stand
Q73678;
Q9-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                       Immunosuppressant polypeptide - has ability to block interleukin-2 response Claim 17; Page 29; 37pp; English.

MAb capable of binding to the gamma chain of the IL-2 recept thus of blocking the IL-2 response, is produced by mouse hyt line GP-2 (FERM BP-4641). DNA encoding the variable region this MAb was expressed in E. coli, yielding Fv(GP-2) with immunosuppressive activity.

Sequence 732 BP; 180 A; 204 C; 182 G; 166 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takeshita T;
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26-OCT-1994.
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           TTGTCCTGCAAAGCTTCTGACTTCAACATTAAAGACTATTATATATCCACTGGGTGAAGCAG
                                                                             GGGACAAAGTTGGAAATAAAAGGTTCTA---CCTCCGGATCTGGTAAATCTTCTGAAGGT
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TIGTCCTGCAAGGCTTCTGGCTACACATTCACCAGCTACTGGATGCACTGGGTGAAGCAG
                                                         AAAGGTGTGCAGCTGCAGCAGTCTGGGGGTTGAGCTTGTCCGAGGAGGGGCCCTTAGTCAAG
                                                                                                                                                                                                                                           ACCTGCACTGCCAGCTCAAGTGTAAGTTCCAGTTACTTGCACTGGTACCAGCAGAAGCCA
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                                     CTGGATCTGAGCTGGTGAGCCTGGAGCTTCAGTGAAG
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                                                                                                                                                                                                                                                                                                                         Query Match
Best Local s
Matches 509
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30-JUN-1992; US-906555.
(MOLE-) MOLECULAR ONCOLOGY I
KASPIZYK PG, King CR;
WPI; 94-025878/03.
P-PSDB; R45442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9400136-A.
06-JAN-1994.
21-OCT-1992;
30-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Fig 7; 37pp; English.

Example; Fig 7; 37pp; English.

The source of human erbB-2 protein for the prodn. of antibodies not a source of human erbB-2 protein on its surface (Ny erbB-2). Abs no. 21 and 23 are directed against the extracellular domain of gp185 erbB-2. Nude mice manipulated to produce rapidly growing tumours were used in a trial of the efficacy of the Abs. animals given a combination of the 2 Abs, tumours completely regressed after 11 days.

Sequence 711 BP; 175 A; 183 C; 187 G; 165 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treatment of malignancies over-expressing ERB-[2 - 2 monoclonal antibodies which recognise different e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence encoding the single chair single chair anti-erbBl antibody;
                                                                                                                                                                                                                                                                                                          C Local S. 509;
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                                                                                                                                         CTTGCAGGGCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCT 127
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09; Conservative
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79.2%;
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: Pred. No. 2e-1
1; Mismatches
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2e-105;
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    epitopes of

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target certs
Disclosure; Fig 3; 26pp; English.

Disclosure; Fig 3; 26pp; English.

The sequence is an NdeI-HindIII fragment encoding the L and H chains of murine MAD OVB3, joined together via a linker. The sequence is present in clone poVB3158-1 in which the 3' end is linked to the 5' end of the coding sequence for PE40, a a Pseudomonas exotoxin lacking domain I. The protein expressed by the clone can be used to kill specific target cells.

Commence 738 BP; 181 A; 193 C; 192 G; 172 T;
                                                                                                                                                                                                  US7463111-A.
28-MAY-1991.
                                                                                                                                                                                                                                                                                                                                                                                                              Q12405;
Q12405;
                                                                                                                                                                                                                                                                                                                                                                            16-SEP-1991 (first entry)
OVB3 light and heavy chains.
Immunoglobulin; immunotoxin;
                                                                                                                                                WPI;
                                                                                                                                                                                                                                                misc_rna
                                                                                                                                                                                                                                                                               misc_rna
                                                                                                                                                                                                                                                                                                               misc_rna
                                                                                                    Rapid cloning of antibody genes as single chain immuno-toxins
by fusing genes with DNA encoding cytotoxic molecules, to kill
target cells
                                                                                                                                      P-PSDB; R12798.
                                                                                                                                                         11-JAN-1990; US-463111.
(USSH ) NAT INST OF HEALTH.
Pastan I;
                                                                                                                                                                                                                                                                                                                                              Key
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370. .729
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/label=
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RESULT T91615 AC TY 15 DT TY 16 DT TY 17 DT TY 1
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Best Loc
Matches
                                                                                         26-AUG-1997.
15-FEB-1996; 027622.
15-FEB-1996; JP-027622.
(TOYJ) TOSOH CORP.
(TOYJ) TOSOH CORP.
WPI: 97-474306/44.
                                                                                                                                                                                                                                               cDNA encoding an anti-gp130 antibody derived scrisingle chain Fv; scFv; antibody; E. coli; anti-T: anti-gp130 antibody; inclusion body; chaperonin; Synthetic.
  Producing single chain Fv antiborancession in an inclusion body co-expression with a chaperonin
                                                                                                                                                                                                 JÕ9220092-A.
26-AUG-1997.
                                                                         P-PSDB; W25784.
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Best Local S
Matches 522
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The sequences given in T91614-15 encode single chain Fv (scFv) antibodies which are produced in E. coli. The scFv's are derived from an anti-T3 antibody or an anti-T9130 antibody and are produced either by: (1) expression as an inclusion body, followed by folding (i.e. by denaturation and solubilisation) or (2) expression as a soluble fraction by co-expression with chaperonin. Using the methods, scFv can be produced in E. coli, either in a soluble fraction or in inclusion bodies. Like the parent double chain antibodies, the scFv polypeptides are useful in immunological diagnosis or for separation and purification, but they lessen the side effects caused by antibody constant regions. The availability of scFv polypeptides contributes to fundamental research and development of diagnostic and therapeutic
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              TGCTTACTATGCTACTACTGGGGTCAAGGAACCTCGGTCACCGTCTCCTCA
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Producing single chain Fv antibody in Escherichia coli - by expression in an inclusion body, followed by protein folding or by co-expression with a chaperonin as a soluble fraction co-expression with a chaperonin as a soluble fraction co-expression with a chaperonin as a soluble fraction of the sequences given in T91614-15 encode single chain Fv (scFv) antibodies which are produced in E.coli. The scFv's are derived crown an anti-T3 antibody or an anti-T9130 antibody and are produced in E.coli. The scFv and are produced cither by: (1) expression as an inclusion body, followed by folding (i.e. by denaturation and solubilisation) or (2) expression as a soluble fraction by co-expression with chaperonin. Using the methods, scFv can be produced in E. coli, either in a soluble fraction or in inclusion bodies. Like the parent double chain antibodies, the scFv polypeptides are useful in immunological diagnosis or for separation and purification, but they lessen the side effects caused by antibody constant regions. The availability of scFv polypeptides contributes to fundamental research and development of diagnostic and therapeutic
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22-DEC-1997 (first entry)
22-DEC-1997 (first entry)
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Single chain Fv; scFv; antibody; E. col
anti-gp130 antibody; inclusion body; cl
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Key
Location/Qualifiers
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Pred. No. 5.5e-78;
D; Mismatches 226
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pos:385. .387,
p codon given"
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E. coli;
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anti-T3 antibody;
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                                                                                              The single chain polypeptide is derived from the mature light and chavy chains of a monoclonal antibody (MAD) and has affinity for a given antigen (Fluorescein). It comprises a first c polypeptide comprising the antigen binding portion of of the light c chain variable region of an antibody and a second polypeptide comprising the antigen binding portion of the heavy chain variable region of an antibody and at least one peptide linker linking the cregion of an antibody and at least one peptide linker linking the first and second polypeptide chains. The resulting single chain c polypeptide can be used in diagnostics, therapy (in vivo and in vitro), imaging, purifications and biosensors. This particular single chain binding molecule was designated 18-2-3/TRY202' and contains one linker peptide.
                           Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                          02-SEP-1986; 902971.
02-SEP-1986; US-902971.
02-SEP-1987; US-902110.
19-JAN-1989; US-299617.
25-APR-1990; US-512910.
                                                                                                                                                                                                                                                                                       Single chain poly:peptide for binding ant and heavy chain antigen binding portions Example 9; Figure 39; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coding sequence of polypéptide with affinity for fluorescein. Monoclonal antibody; MAD; affinity; binding; antigen; diagnos therapy; imaging; purification; biosensors; ss. synthetic.
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                                                                                                                                                                                                                                                                                                                                                   Bird RE, Hardman K, WPI; 93-367875/46.
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 GCTGACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAAAAGGTCACCATGACCTG
                           al Similarity 68.7
493; Conservative
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Pred. No. 8e-77;
0; Mismatches 210;
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                                                                                                                           Key
                                                                                                                                                   Chimeric
                                                                                                                                                                         18-2-3/TRY202'; ss.
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US5534621-A.
09-JUL-1996.
02-SEP-1986;
02-SEP-1986;
02-SEP-1987;
19-JAN-1989;

902971. US-902971. US-092110. US-299617.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immuno:purifich. using single binding chain molecule including antigen-binding parts of antibody light and heavy chain variable regions connected by a linker - is smaller, stabler and less expensive than complete antibodies

Example 9; Fig 39; 78pp; English.

A DNA construct (713739) codes for single chain binding molecule in-2-3/TRY202/2 (R99649), in which VL and VH regions of anti-cliner composed primarily of alternating Gly and Ser residues, with inker composed primarily of alternating Gly and Ser residues, with expressed in E.coli. Soluble, folded chain antibody (SCA) was expressed in E.coli. Soluble, folded chain antibody (SCA) was obtd. which was capable of exhibiting a biological binding activity equivalent in specificity and affinity to that of a monoclonal antibody. The SCA has the advantages of smaller size, greater stability and reduced cost.

Sequence 720 BP; 180 A; 184 C; 175 G; 181 T;
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Best Local Sin
Matches 493;
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Bird RE,
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01-APR-1993; US-040440.
06-JUN-1995; US-468992.
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RE, Hardman K,
96-333309/33.
                  GCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGCTTCTTATTACTACTA
                                                                                                                                                                                                                                                                                                                                                                                                   CAAGCTTGAGCTGGAAGGTAAATCTTCTGGTTCTGG-----TTCCGAATCTAAATCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGTGCCAGCTCAAGTGTA-----AGTAACATGCACTGGTATCAGCAGAAGTCAAGCAC
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*NATGAACAGTCTGCAAAATGATGACACAGCCATATACTACTGTGCCAAACGACTGGAACG
                                                                                                     GAAATTCCAGGGCAAGGCCAGTATAACAGCAGAGAGATCCTCCAACGCGGCCTACCTTCA
                                                                                                                                                                                                                                        CACTGTCTCTGGGTTTTCATTAACCAACTATGGTGTACACTGGGTTCGCCAGCCTCCAGG
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                                                                                                                                                           AAAGGGTCTGGAGTGGCTGGGAGTAATATGGGCTGG---TGGAAACACAAATTATAATTC
                                                                                                                                                                                                  ACAGGGCCTGGAATGGATTGGATGGATTCATCCTGAGAATGGTAATACTGTATATGACCC
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                                                                              AGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAATTCCAAGAGCCAAGTTTTCTTAAA
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Pred. No. 8e-77;
0; Mismatches 21(
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Best Local S
Matches 493
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Example 9; Fig 39A-B; 78pp; English.

Computer-designed construct 18-2-3/TRY202' (W02191), encoded by the DNA sequence given in T36463, comprises the variable regions of the light and heavy chains of anti-fluorescein monoclonal antibody (Mab) 18-2-3 linked by a peptide designed to fit into a groove on the backside of the variable domain structure. The 18-2-3 VH and VL regions were obtd. by CR amplification of hybridoma RNA, and the DNA construct was inserted into vector pGX3703 and introduced into E. coll. 18-2-3/TRY202' was expressed as a single chain molecule. It exhibited biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5518889-A.
21-MAY-1996.
02-SEP-1986; 902971.
02-SEP-1986; US-902971.
02-SEP-1987; US-092110.
19-JAN-1989; US-299617.
25-APR-1990; US-512910.
01-APR-1990; US-404040.
06-JUN-1995; US-468988.
(ENZO-) ENZON LABS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-2-3/TRY202' single chain binding protein-encoding Antibody engineering; monoclonal antibody; MAD; single chain antibody; immunoassay; fluorescein; 18-2 single chain binding protein; ss.
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Bird RE, Hardman K,
WPI; 96-259060/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric Mus musculus;
Chimeric synthetic.
Key Locations 658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T36463;
                                                                                                                                                                                                                                                                                                         binding activity equivalent in specifically and that of the original MAD.
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18-2-3/TRY202' single chai
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                         CAGTGGCAGTGGGTCTGGAAACTCTTACTCTCTCACGATCAGCAGCATGGAGGCTGAAGA
                                                                                        CTCCCCCAAACTCTGGGTTTATGACACATCCAAACTGGCTTCTGGAGTCCCAGGTCGCTT
                                                                                                                                          TGCTGCCACTTATTATTGTTATCAGGGGAGTGGGTACCCATTCACGTTCGGCTCGGGGAC
                                                                                                                             CAGGGCCAGCTCAAGTGTAAGTTCCAGTTACTTGCACTGGTACCAGCAGAAGTCAGGTGC
                                                                                                                                                                               GCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAAAAGGTCACCATGACCTG
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                                                                                                                                                                                                                                           44.78;
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                                                                                                                                                                                                                                                                                               180 A;
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Pred. No. 8e-77
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Matches 492
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02-SEP-1986;
02-SEP-1987;
19-JAN-1989;
                                                                                                                The sequence was constructed from the variable regions of an antifluorescein MAD, 18-3-2, an IgM. The VI and VH CDNA sequences were synthesised by priming on RNA isolated from hybridona cells. The sequence encodes a single chain binding molecule comprising the variable regions of heavy and light chains linked by peptides. The peptide linker was computer-designed to fit inyo a groove on the backside of the variable domain structure and is composed primarly of alternating Gly and Ser residues. Glu and Lys residues are included to enhance solubility.

See also Q05708-005719.

Sequence 724 BP; 180 A; 186 C; 174 G; 184 T;
                                                                                                                                                                                                                                                                                     P-PSDB; R06482.
Single polypeptide chain bir
variable region of antibody
                                                                                                                                                                                                                                                                                                                                (GENE-) GENEX CORP.
Ladner RC, Bird RE,
WPI: 90-260350/34.
                                                                                                                                                                                                                                                                 variable region.
Disclosure; Fig 39; 68pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JAN-1991 (
18-2-3-/TRY202
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Q05714;
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             GCTGACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAAAAGGTCACCATGACCTG
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GCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAAAAGGTCAACATGACCTG
                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                        ; US-902971.
; US-092110.
; US-299617.
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                              RE, Hardman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                               44.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      variable
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                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                        nding molecules
linked by pepti
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                                                  0
                                                  Score 321.6; DB 1;
Pred. No. 1e-76;
0; Mismatches 209;
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Q51538;
23-MAY-1994 (fi
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277. .279
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166. .168
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                    /transl_except=
484. .486
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280. .282
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274. .276
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PI Bird RE, Hardman K, Ladner RC;

Bird RE, Hardman K, Ladner RC;

DR #P5DB; R43677.

PT Single chain poly:peptide for binding antigen - comprising light and heavy chain antigen binding portions linked by peptide linker and heavy chain antigen begins and an antibody (MAb) and has affinity CC for a given antigen (Bovine growth hormone). It comprises a first CC polypeptide comprising the antigen binding portion of of the light CC chain variable region of an antibody and a second polypeptide comprising the antigen binding portion of the heavy chain variable region of an antibody and a second polypeptide comprising the antigen binding portion of the heavy chain variable comprising the antigen binding portion of the heavy chain variable cregion of an antibody and at least one peptide linker linking the cregion of an antibody and at least one peptide linker linking the colypeptide can be used in diagnostics, therapy contains one linker peptide.

So Sequence 741 BP; 172 A; 188 C; 192 G; 189 T;
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Best Local Similarity
Matches 504; Conser
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09-NOV-1993.
02-SEP-1986; 902971.
02-SEP-1986; US-902971.
02-SEP-1987; US-092110.
19-JAN-1989; US-295617.
19-JAN-1989; US-512910.
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AGACAGTGTGAAGGGGCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTGTACCT
                            CCCGAAATTCCAGGGCAAGGCCAGTATAACAGCAGACACATCCTCCAACGCGGCCTACCT
                                                                                                                     CTGTGCAGCCTCTGGATTCACTTTCATTAGCTATGGCATGTCTTGGGTTCGCCGAACTCC
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Pred. No. 1.3e
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pr immuno:purificn. using single binding chain molecule including practices antigen-binding parts of antibody light and heavy chain variable presents connected by a linker is smaller, stabler and less presents than complete antibodies

Presents than complete antibodies

Example 3; Fig 28; 78pp; English.

A DNA construct (T13737) codes for single chain binding molecule TRT59 (R99647), in which amino acids (aa) 1-105 of the VL region of anti-bovine growth hormone mouse IgG1 monoclonal antibody 3C2 and aa2-123 of the 3C2 VH are joined by a peptide linker from the TV region of the 13A anti-phosphorylcholine myeloma antibody MCPC-603. The construct was expressed in E.coli. Single chain binding molecules retain the specificity of the heavy and light chain aggregate variable region of the native antibody but have the advantages of smaller size, greater stability and reduced cost.

Sequence 741 BP; 172 A; 188 C; 192 G; 189 T;
                                                                                                                                                                                                                                                           US5534621-A.
09-JUL-1996.
02-SEP-1986;
02-SEP-1987;
02-SEP-1987;
19-JAN-1989;
25-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-OCT-1996 (first entry)
Single chain binding molecule TRY59 DNA.
Antibody engineering; single polypeptide chain binding molecule;
heavy chain; light chain; monoclonal antibody; MAb;
bovine growth hormone; bGH; immunoaffinity purification; TRY59;
Chimeric synthetic.
                                                                                                                                                                                    Bird RE, Hardman K, Ladner WPI; 96-333309/33. P-PSDB; R99647.
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06-JUN-1995;
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US-092110.
US-299617.
US-512910.
US-040440.
US-468992.
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274. .27
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277. .279
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166.168
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280. .282
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Query Match Best Local Sim Matches 504;

Similarity

44.68;

Conservative

0,

Score 321.2; Pred. No. 1.3e 0; Mismatches

3e-76; DB 1;

Length

18;

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CGTCTCCTAA 741
                                                        TACGGTAGTACTTACGGATTACTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCAC
                                                                       TACTATAGT-----GCTTACTATGCTATGTACTACTGGGGTCAAGGAACCTCGGTCAC
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Search completed: May 13, Job time: 1188 sec 1999, 09:55:30 Ş 멍 δÃ 밁 δÃ

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd
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OM protein protein search, using sw model

Run

May 13, 1999, 09:40:48; Search time 21.53 Seconds (without alignments) 412:360 Million cell up

cell updates/sec

Perfect score: US-08-704-178-3 1267

Sequence: MDLQLTQSPAILSASPGEKV.....RRVTDWYFDVWGAGTTVTVS

Scoring table: BLOSUM62

Searched: 116738 seqs, 37460341 residues

4:2: pir2:* pir4:* pir1:*

Database

PIR_58:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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•	Ig heavy chain V r	ig light chain V r	Ig heavy chain V r	Ig heavy chain V r	Ig kappa chain pre

ALIGNMENTS

RESULT PC4402

hapten-specific single-chain antibody variable fragment and alkaline phosphatase C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 03-Sep-1998 #sequence_revision 03-Sep-1998 #text_change 03-Sep-1998 C;Accession: PC4402 C;Accession: PC4402 R;Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune, T. J. Biochem. 122, 322-329, 1997 J. Biochem. 122, 322-329, 1997

A;Title: Construction, bact bacterial expression, and characterization of hapten-specific

A; Reference number: PC4 A; Accession: PC4402 A; Status: preliminary A; Residues: 1-287 <SUZ>

Query Match 48.6 Best Local Similarity 51.0 Matches 132; Conservative 48.68; 32; Score 615.5; DB 3; Pred. No. 3.5e-38; Length 287; Indels 25; Gaps 6;

B ş 23 MDIQAVVTQESA-LTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNR 81 1 MDLQ--LTQSPAILSASPGEKVTMTCR----ATPSVSYMHWYQQKPGSSPKPWIYTTSNL 54

밁 Š 82 55 ASGVPARFSGGGSGTSYSLTYSRYEAEDAATYYCQQWSRSPPTFGGGSKLEIKGSTSGSG 114 APGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLSSADDAK 141

ğ В 142 115 KDDAKKDDAKKDDAKKDGQVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPG KSSEGKG------VQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHG 162 201

163 KNLEWIGLINPYNGDTNYNQKFKGKATFTYDKSSSTAYMELLSLTSEDSAYYYCARRYTD 222

δã Вb 202 RGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAR--YD

259

QΥ 223 W----YFDVWGAGTTVTVS 237

밁

260 YYGSSYFDYWGQGTTLTVS 278

RESULT 2
PH0887

Ig heavy chain V region (anti-CD3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 16-Aug-1996
C;Accession: PH0887
R;Shalaby, M.R; Shepard, H.M.; Presta, L.; Rodrigues, M.L.; Beverley, P.C.L.; Feldma
J. Exp. Med. 175, 217-225, 1992
A;Accession: PH0887
A;Reference number: PH0885; MUID:92113462
A;Accession: PH0887
A;Accession: PH0887
A;Accession: PH0887
A;Accession: PH0887
A;Rote: the authors translated the codon TTC for residue 70 as Leu
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

42.6%; 85.0%;

Query Match Best Local Similarity Matches 102; Conserv Conservative Score 540; DB 2; Pred. No. 4.2e-33; 6; Mismatches 8 Length 122; Indels 4. Gaps

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Ig heavy chain V region (MOPC 104E) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Nov-1979 #sequence_revision 14-Nov-1983 #text_change 16-Aug-1996
C:Accession: A02039
R:Kehry, M.R.; Fuhrman, J.S.; Schilling, J.W.; Rogers, J.; Sibley, C.H.; Hood, I Biochemistry 21, 5415-5424, 1982
A:Tittle: Complete amino acid sequence of a mouse mu chain: homology among heavy A;Reference number: A02039; MUID:83075344
A;Accession: A02039
A;Molecule type: protein
A;Residues: 1-117 <KEH>
C:Comment: The glycosylated asparagine residue does not have the usual N-X-S/T C:Comment: This protein binds dextran.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein; heterotetramer; immunoglobulin formology
F:15-98/Domain: immunoglobulin homology <IMM'>
F:22-96/Disulfide bonds: #status predicted
F:55/Binding site: carbohydrate (Asn) (covalent) #status atypical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region (129) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-199
C:Accession: 137267
R:Rfff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and 11ght chain variable region sequences and antibody prop
A:Reference number: A38740; MUID:91177923
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-128 <RUF>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>
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                  122 VQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGLINPYNGDTNYN 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGLINPYNGDTNY 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NQKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCARR-----VTDWYFDVWGAGTTV 234
95;
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Pred. No. 5.2e-30;
0; Mismatches 12
                                                         Score 496.5; DB
Pred. No. 6e-30;
9; Mismatches
                                                                                            DB 1;
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                                                           Indels
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RESULT
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Ig heavy chain V region (Py69) - mouse
C; Species: Mus musculus (house mouse)
C; Date: 18 - oct-1991 **sequence_revision 18 - oct-1991 **text_change 16 - item is the content of the conte
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C:Date: 10-Nov-1997 *sequence_revision 23-Jan-1998 *te C:Accession: PC4405
R;Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.
Chinese BioChem. J. 12, 648-653, 1996
A;Title: Generation of a phage display library of the A;Reference number: PC4405
A;Accession: PC4405
A;Accession: PC4405
A;Experimental source: spleen cell
C:Superfamily: immunoglobulin V region; immunoglobulin
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                              FSGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIK 107
                                                                                                                                                   DLQLTQSPAILSASPGEKVTMTCRATPSVSYMHWYQQKPGSSPKPWIYTTSNLASGVPAR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TVS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVQLQQSGPELVKPGASMKISCKTSGYTFTEYIMHWVKQSHGKSLEWIGRFNPNSGGSTY 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRGPYGNYYTSYYFDYWGQGTTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NQKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCARR-----VTDWYFDVWGAGTTV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDY-DWYFDVWGAGTTVTVS 116
FSGSGSGTSYSLTISRVEAEDAATYYCQQWRDNPPTFGGGTKLEIK
                                                                                                                    DIELTQSPAIMSASPGEKVTMTCSASSSISYMHWYQQKPGTSPKRWIYDTSKLASGVPAR
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                                                                                                                                                                                                                                        ; 68
                                                                                                                                                                                                                                                                    Similarity
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Pred. No. 8.5e-30;
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No. 1.6e-29;
                                                                                                                                                                                                                                                                                                                                                                                     immunoglobulin
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Ab2s

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A; Molecule type: protein
A; Residues: 1-117 <SCH>
A; Residues: 1-117 <SCH>
A; Note: the sequences of 10 hybridoma proteins that als
C; Comment: This protein binds dextran.
C; Superfamily: immunoglobulin V region; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-120 <SIM>
A; Note: sequence extracted
C; Superfamily: immunoglobul
C; Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, J. Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies that dia;Reference number: A45722; MUID:93100833
A;Accession: E45722
Ig kappa chain V region (2D3) - mouse C;Species: Mus musculus (house mouse) C;Date: 07-Jun-1990 #sequence_revision C;Accession: PLOU82 R;Meek, K.; Hasemann, C.; Pollok, B.; J. Exp. Med. 169, 519-533, 1989
                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: heterotetramer; hybridoma; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM> F;22-96/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Schilling, J., L., R;Schilling, J., L., 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-May-19
C;Accession: E45722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Amino acid sequence A;Reference number: A26242; NA;Accession: A26242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain V region (J558) - mouse C; Species: Mus musculus (house mouse) C; Date: 30-Jun-1991 #sequence_revision C; Accession: A26242
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Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 VQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGL-INPYNGDTNY 180
                                                                                                                                                                                182 QKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCARRVTDWYFDVWGAGTTVTVS
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                                                                                                                                                                  QKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARD-RYWYFDVWGAGTTVTVS
                                                                                                                                                                                                                                 VQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NQKFKGKATLTVDKSSNTAYMELLSLTSADSAVYYCTRRGFRDYSMDYWGQGTSVTVS
                                                                                                                                                                                                                                                                                                 . Similarity
93; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clevinger, B.;
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Pred. No. 1.8e-29;
                                                                                                                                                                                                                                                                                               Score 487.5; DB 1
Pred. No. 2.7e-29;
Mismatches 13
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                  Alkan,
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                                               07-Jun-1990 #text_change 16-Aug-1996
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                 Slaoui, M.;
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Ig heavy chain precursor V region (BXW16) - C;Species: Mus musculus (house mouse) C;Date: 21-May-1990 #sequence_revision 31-De
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avda J. Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies A;Reference number: A45722; MUID:93100833
A;Accession: F45722
A;Status: preliminary; not compared with con A;Molecule type: nucleic acid
A;Residues: 1-120 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-137 <KOF>
A; Cross-references: GB: M20831; NID: g196949; PID: g196950
C; Superfamily: immunoglobulin V region; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
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C; Keywords:
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A; Note: the sequence shown
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A; Residues: 1-106 <MEE>
                                                                                                                                       anti-glycoprotein H monoclonal antibody heavy-chain variable domain C;Species: Mus musculus (house mouse) C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-MC;Accession: F45722
                                                                                                                                                                                                             RESULT
F45722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Clin. Invest. 82, 852-860, 1988
A; Title: Immunoglobulin kappa light chain
A; Reference number: A94689; MUID:88331394
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R; Kofler, R.; Stroh
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Best I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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                                                                                                                                                                                                                                                                               TLTVS
                                                                                                                                                                                                                                                                                                                  TVTVS 237
                                                                                                                                                                                                                                                                                                                                                                                                                      AGVHSE---IQLQQSGAELVKPGASVKISCKASGYSFTGYNMNWVKQSHGKSLEWIGNIN
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74.48;
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Pred. No. 6.1e-29;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 480.5; DB Pred. No. 1e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                      Avdalovic,
                                    conceptual translation
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                                                                                                                        Au,
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                                                                                      antigenic
                                                                                                                                                                                           (Mab
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                                                                                                                                                                                                                                                                                                                                                                                    232
                                                                                                                                                                                                                                                                                                                                                                                                                      71
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                                                                                                                      M.S.;
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                                                                                         A:Molecule type: DNA
A:Residues: 1-135 </RAO>
A:Residues: 1-135 </RAO>
A:Residues: 1-135 </RAO>
A:Residues: FID:00307; NID:g220448; PID:d1000661; PID:g220449
A:Cross-references: GB:D00307; NID:g220448; PID:d1000661; PID:g220449
A:Note: the authors translated the codon AAG for residue 32 as Asn and GAC for 92 as Gly C:Comment: The gene encoding this protein was isolated from a hybridoma that produces an C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin predicted <SIG>
F:1-19/Domain: signal sequence #status predicted <NAT>
F:20-135/Product: Ig heavy chain V region PAR #status predicted <NAT>
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C;Superfamily: immunoglobulin V region; im
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Decies: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 17-Apr-1998
C:Accession: S26319
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
                                                                                                                                                                                                                                                                                       R;Yaoita, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, T. J. Blochem. 104, 337-343, 1988
A;Title: Blased expression of variable region gene families A;Reference number: PSO057; MUID:89197817
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A; Residues: 1-114 <STA>
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C;Accession: PS0057
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Best Local S
Matches 91
                                                                                                                                                                                                                                                                                                                                                                                                           j heavy chain precursor V region (PAR) - mouse
;Species: Mus musculus (house mouse)
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Best Local :
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 QESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGLINPYNGDTNYNQKF 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQSGPELVKPGASVKISCKASGYSFTGYFMNWVKQSHGKSLEWIGRINPYNGDTFYNQKF
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Pred. No. 1.6e
l1; Mismatches
              Score
Pred.
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            474.5;
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.6e-28;
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.8e-28;
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A; Molecule type: mRNA
A; Residues: 1-119 <EIL>
C; Superfamily: immunoglobulin V region; immC; Keywords: heterotetramer; immunoglobulin
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C;Species: Mus musculus (house mouse)
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 16-Aug-1996
C;Accession: PH0099
R;Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesniau
Mol. Immunol. 27, 1029-1038, 1990
A;Title: Analysis of the structural diversity of monoclonal antibodies to c;
A;Reference number: PH0087; MUID:91042649
A;Accession: PH0099
                                                                                                                                                                                                                                                        C;Accession: F30502
R;Eilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A;Title: V region sequences of anti-DNA and A;Reference number: A30502; MUID:88315787
A;Accession: F30502
                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region (A52) - mouse C; Species: Mus musculus (house mouse) C; Date: 03-Nov-1988 #sequence_revision
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A; Residues: 1-119 <SCH>
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                                                                                                                                                                                                                                         A; Status: preliminary
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Best Local
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Best Local Similarity
113
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                                                                                           Similarity
                                                                          Conservative
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                                                                                         37.3%;
77.1%;
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78.0%;
                                                                                         Score 473; DB 2;
Pred. No. 3.1e-28;
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Pred. No. 2.9
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                                                                          14;
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ALIGNMENTS

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

Run OM protein protein search, using sw model

May 13, 1999, 09:55:33; Search time 16.53 Seconds (without alignments).
384.825 Million cell updates/sec

Title:

Perfect score:

Sequence: US-08-704-178-3
1267
1 MDLQLTQSPAILSASPGEKV.....RRVTDWYFDVWGAGTTVTVS 237

Scoring table: BLOSUM62

Searched: 74019 segs, 26840295 residues

Database : SwissProt_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8 8 Q	SO	W H F	뮸뮸	გგ	3 S	RA :	Z Z	R R	8	88	SE	DT	Į,	A	RESULT HV12_M
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vai	AA; 1	LIN V REGIO	2; MHMS4E.	ALSO BEEN DETERMINED. THIS PROTEIN BINDS DEXTRAN.	UENCE OF TH		075344. FUHRMAN J.		ODENTIA.	METAZOA; CH	AIN V REGIO	(REL. 20,	(REL.	į	STANDARD;
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HY13 LUF HY14 LUF HY15 LUF HY1 HV13_MOUSE

HV13_MOUSE

STANDARD;

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117 AA.

RC P01757;

YT 21-JUL-1986 (REL. 01, CREATED)

YT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

YT 01-NOV-1991 (REL. 20, LAST ANOOTATION UPDATE)

YT 01-NOV-1991 (REL. 20, LAST ANOOTATION UPDATE)

YE IG HEAVY CHAIN V REGION (J558).

YOUS MUSCULUS (MOUSE).

CE EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

CE CUTHERIA; RODENTIA.

N 11. SEQUENCE.
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MEDILINE; 80078170.
SCHILLING J., CLEVINGER B., DAVIE J.M., HOOD L.;
SCHILLING J., CLEVINGER B., DAVIE J.M., HOOD L.;
NATURE 283:35-40(1980).
-1- THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN THE D AND J SEGMENTS.
-1- THIS PROTEIN BINDS DEXTRAN.
PIR; A26242; MHMSJ5.
HSSP; P01789; 2FGW. DISULFID IMMUNOGLOBULIN V REGION. DISULFID 22 96 BY SIMILARITY.

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 SEQUENCE FROM N.A. MEDLINE; 82222262. KNAPP M.R., LIU C.- BLATTNER F.R.;
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DILDROP R., BOVENS J., SI
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p01759;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UP:
01-FEB-1991 (REL. 17, LAST ANNOTATION |
1G HEAVY CHAIN PRECURSOR V REGION (BCL.
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EMBL: J00494; G195011; -.
PIR; A02042; HYMSB1.
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IMMUNOGLOBULIN V REGION; S
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13-AUG-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
1G KAPPA CHAIN V-VI REGION (NO2-17.4.1).
MUS MUSCULIS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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                                                                                                                                                                                                                                                                                                                                               11561
                                                                                                                                                                                                                                                                        34.58;
77.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYBRIDOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL.
                                                                                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₩;
                                                                                                                                                                                                                                                   ; Score 437; DI
; Pred. No. 1.40
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OXAZOLONE
                                                                                                                                                                                                                                                                                                                                                                                FRAMEWORK BY SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY - DETERMINING FRAMEWORK 2.
COMPLEMENTARITY - DETERMINING FRAMEWORK 3.
COMPLEMENTARITY - DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 439.5;
Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAMEWORK
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                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MARKHAM
                                                                                                                                                                                                                                                                                                                                             1BC0C1E3
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                  107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PHOX)
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MILSTEIN ANTIBODY

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Best Local S
Matches 79
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13-AUG-1987 (REL. 05,
01-OCT-1993 (REL. 27,
1G KAPPA CHAIN V-VI F
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE: 83271467.
KAARTINEN M., GRIFFITHS G.M.
NATURE 304:320-324(1983).
-!- FUNCTION: ANTI-2-PHENYL
EMBL; K00740; G196445; -.
   DOMAIN
DISULFID
NON_TER
SEQUENCE
                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
1G KAPPA CHAIN V-VI REGION (NG6-8.3.1).
MUS MUSCULUS (MOUSE).
EUKARXOTA; METAZOA; CHORDATA; VERTEBRATA; TETI
                                       DOMAIN
                                                                                                                                                                                                                                                      MOUSE
                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUTHERIA; RODENTIA.
                                                                                 DOMAIN
                                                                                                                           KAARTINEN M., GRIFFITHS G.M., NATURE 304:320-324(1983).
                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 83271467.
                                                                                                                                                                                MUS MUSCULUS (MOUSE) EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                            KV6G_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                       EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMUNOGLOBULIN V
                                                                                          IMMUNOGLOBULIN
                                                                                                   !- FUNCTION: ANTI-2-PHENYL MBL; K00737; G196439; -. SSP; P01679; 1FVB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P01679;
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107
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49
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106
107
11556
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                                                                                         REGION;
                                                                                                                                                                                             05, CREATED)
05, LAST SEQUENCE UPDATE)
27, LAST ANNOTATION UPDATE)
VI REGION (NQ2-48.2.2).
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33
48
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87
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106
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CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                               CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                       11572
                                                                                                                                                                                                                                                                                                                                                                    34.1%;
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                                                                                          HYBRIDOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYBRIDOMA
                                                                                                                                                                                                                                                                                                                                                                                                       Æ;
    MW;
                                                                                                                    OXAZOLONE
                                                                                                                                                                                                                                                                                                                                                            Score 432; DB
Pred. No. 3.3e
L1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OXAZOLONE
                                                                                                                                                                                                                                                                                                                                                                                                                        FRAMEWORK 3.

COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING
                     COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
BY SIMILARITY.
                                              COMPLEMENTARITY-DETERMINING FRAMEWORK 3.
                                                                COMPLEMENTARITY-DETERMINING FRAMEWORK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING
                                                                                 FRAMEWORK 1.
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                                                                                                                                     MARKHAM
                                                                                                                                                                                                                                            PRT;
    1AB8295D CRC32;
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                                                                                                                                                                                                                                                                                                                                                                    2 432;
3.
                                                                                                                                                                                                                                             107
                                                                                                                                     A.F.,
                                                                                                                   (PHOX) ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PHOX)
                                                                                                                                                                                                                                                                                                                                                                     DB 1;
.3e-26;
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                                                                                                                                     MILSTEIN C.;
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                                                                                                                                                                                                                                                                                                                                                             13;
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                                                                                                                                                                                                                                                                                       106
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RESULT 8
KV6H_MOUSE
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                           13-AUG-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUE
13-AUG-1993 (REL. 27, LAST ANNO?
1G KAPPA CHAIN V-VI REGION (NO5-
MUS MUSCULUS (MOUSE).
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
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Best Local
                                                                                                                _MOUSE
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DISULFID
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 83271467.

KAARTINEN M., GRIFFITHS G.M., MARKHAM A.F., MILSTEIN C NATURE 304.320-324 (1983).

-I- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY. EMBL; K00739; G196443; -.

EMBL; K00739; G196443; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDA:
01-OCT-1993 (REL. 27, LAST ANNOTATION UPI
IG KAPPA CHAIN V-VI REGION (NQ5-61.1.2).
                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
         SEQUENCE FROM N.A. MEDLINE; 83271467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KV6H_MOUSE
KAARTINEN M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 83271467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUTHERIA;
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                                                                                                                                                                         GGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIK
                                                                                                                                                                                                ITQSPAIMSASPGQKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLDSGVPARPSG
                                                                                                                                                                                                              LTQSPAILSASPGEKVTMTCRATPSVSYMHWYQQKPGSSPKPWIYTTSNLASGVPARFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTQSPAIMSASPGQKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPARFSG
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                                                                                                                                                                                                                                                                                                            23
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23
GRIFFITHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                     7 REGION;
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106
107
107
11605;
                                                                                                                                                                                                                                                  34.0%;
76.7%;
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76.7%;
G.M.,
                                                                                                                                                                                                                                                                                        MW;
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                                                                SEQUENCE UPDATE)
ANNOTATION UPDATE)
(NQ5-78.2.6).
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Pred. No. 4e-2
L1; Mismatches
                                                                                                                                                                                                                                                Score 431; DB 1
Pred. No. 4e-26;
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 2.
                                                                                                                                                                                                                                                                                                          FRAMEWORK 3.

COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
BY SIMILARITY.
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                                                                                                                 PRT;
MARKHAM A.F.,
                                               VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                        1CF3CE8D CRC32;
                                                                                                                                                                                                                                        Mismatches
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                                                                                                                A
                                               TETRAPODA;
MILSTEIN
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                                               MAMMALIA;
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Best Local S
Matches 81
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Best Local S
Matches 79
                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 83271467.
KAARTINEN M., GRIFFITHS G.N.
MATURE 304:320-324(1983).
EMBL; K00746; G554059; -.
HSSP; P01679; IBAF.
IMMUNOGLOBULIN V REGION; H)
                                                                                                                                       DOMAIN
DOMAIN
DOMAIN
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NON_TER
SEQUENCE
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DOMAIN
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DOMAIN
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13-AUG-1987 (REL. 05, LAST SEQUENCE UP
01-OCT-1993 (REL. 27, LAST ANNOTATION
1G KAPPA CHAIN V-VI REGION (NQ2-6.1).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRA
                                                                                                                         DOMAIN
                                                                                                                                DOMAIN
                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                      KV6K_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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FUNCTION: ANTI-2-PHEN
L; K00744; G196453; -.
P; P01679; 1FVB.
                                                                                                                                                                                                                                                                                                                                                                       GGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIK 107
SGSATSYSLTITRMQAEDAATYYCQQWSSYPPMLTFGAGTKLELK
                                                                                                                                                                                                                                                                                                                                           GGSGTSYSLTVSRVEAEDAATYYCQQWSRSPP--TFGGGSKLEIK 107
                                                           Similarity 77.1
81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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11611 MW;
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                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                REGION;
23
33
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108
87
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11713
                                                                                                                                                                                                                                                CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                              33.98;
                                                                   33.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -PHENYL
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G
                                                                                                                                                                             HYBRIDOMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYBRIDOMA
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;
                                                                                                 , WM
                                                          ; Score 429; DI
; Pred. No. 5.76
11; Mismatches
                                                                                                               COMPLEMENTARITY-DETERMINING 1
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2
FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3
FRAMEWORK 4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                       Score 430; DB
Pred. No. 4.7e
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OXAZOLONE (PHOX) ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPLEMENTARITY-DETERMINING FRAMEWORK 2.
                                                                                                                                                                      FRAMEWORK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAMEWORK 1.
                                                                                                                                                                                                           MARKHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                             E926BBEB CRC32;
                                                                                                 8B48A204 CRC32;
                                                                                                                                                                                                                                                                                                      108
                                                                                                                                                                                                           A.F.,
                                                                                                                                                                                                                                                                        UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                              ); DB 1;
4.7e-26;
                                                           DB 1; 1
5.7e-26;
hes 11;
                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                 TETRAPODA;
                                                                                                                                                                                                           MILSTEIN
                                                                         Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 107
                                                                                                                                                                                                                                                                                                                                            106
                                                           Indels
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                                                                                                                                                                                                                                                 MAMMALIA;
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                                                          Gaps
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HVO3_WM HVO3_W
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HV14_MOUSE
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                                                                                          Query Match
Best Local S
Matches 80
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Best Local S
Matches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE; 83131846

SIEKEVITZ M., GEFTER M.L., BRODEUR P.,

MARSHAK-ROTHSTEIN A.;

EUR. J. IMMUNOL. 12:1023-1032(1982).

-!- FROM ANALYSIS OF THE SIZES OF SEVE

THAT HYBRIDIZE TO THIS ONE, THE AU

THESE V REGIONS HAVE REARRANGED TO

PIR; A02028; HYMSG7.

HSSP; P01789; 6FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HV03_MOUSE
HV03_MOI
P01747;
                                                                                                                                                                                                                                            CHAIN
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLISS;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TG HEAVY CHAIN PRECURSOR V REGION (108A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                        IMMUNOGLOBULIN V REGION;
SIGNAL 1 19
CHAIN 20 117
NON_TER 117 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 81245215.
GIVOL D., ZAKUT R., EFFRON
NATURE 292:426-430(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG HEAVY CHAIN PRECURSOR V REGION (108A).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUE)
21-JUL-1986 (REL. 01, LAST ANNOT:
IG HEAVY CHAIN V REGION (36-65).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HV14_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY;
NON_TER 120 120
SEQUENCE 120 AA; 13307 MW; BBA8CCA1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUTHERIA; RODENTIA.
                                  113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                           A02041; HVMS8A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGKSSEGKGVQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGLIN 172
                                                                                                                                                                                                                                                                                                                                                                                                     P01789; 1IGI
                                                                                          ;08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 68.
                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RODENTIA.
                                                                                                                                                                                                                                   20
117
117
                                                                                          Conservative
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K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                   33.3%;
                                                                                                                                                                                                                                               12972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.5%;
68.1%;
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, LAST SEQUENCE UPI
, LAST ANNOTATION (
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                                                                                       Score 422; DB Pred. No. 2.1e 8; Mismatches
                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 424.5;
Pred. No. 1.4e
4; Mismatches
                                                                                                                                                                                                                                                                                                       IG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RECHAVI
                                                                                                                                                                                                                                            941C002E CRC32;
                                                                                                                                                                                                                                                                                                       HEAVY CHAIN V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEVERAL OTHER DIFFERENTIATED HE AUTHORS CONCLUDE THAT ALL CENTROLE THE SAME J SEGMENT, JH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G.,
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les 21;
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                                                                                                                      .1e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAM
                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::
                                                                                                                                                                                                                                                                                                       REGION
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                                                                                                                                                  Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 120;
                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COHEN
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                                                                                          Gaps
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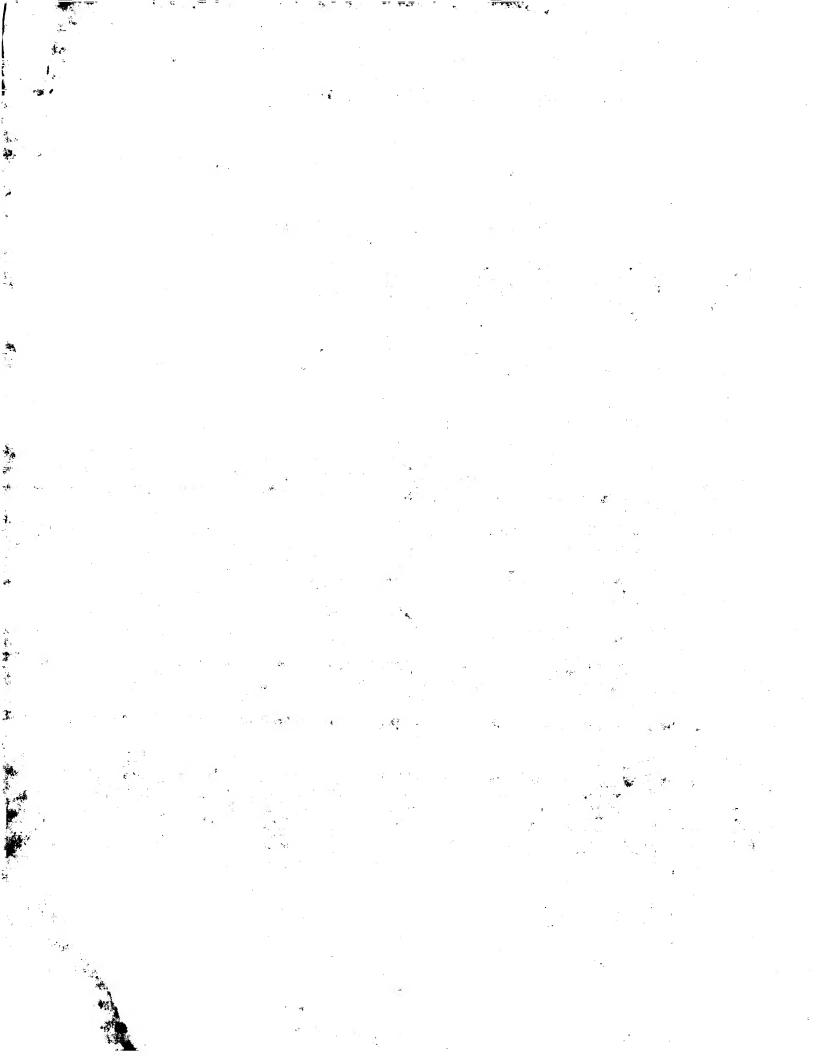
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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21-JUL-1986 (REL. 01, LAST SEQUE
01-OCT-1993 (REL. 27, LAST ANNOT
IG KAPPA CHAIN V-VI REGION (XRPC
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VI
                                                                                                                                                                                                                                                                                                                  KV6A_MOUSE P01675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KV6D_MOUSE P01678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RUDIKOFF S., RAO D.N., GLAUDEMANS C.P.J., POTTER M.; PROC. NATL. ACAD. SCI. U.S.A. 77:4270-4274(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
                                                                     RAO D.N., RUDIKOFF S., POTTER M.;
BIOCHEMISTRY 17:5555-5559(1978).
-!- THIS CHAIN WAS ISOLATED FROM
                                                                                                            MEDLINE; 79082830.
RAO D.N., RUDIKOFI
                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 81054757.
RUDIKOFF S., RAO D.
PROC. NATL. ACAD. S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG KAPPA CHAIN V-VI REGION (SAPC
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UP
01-OCT-1993 (REL. 27, LAST ANNOTATION
                                                                                                                                                 SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                      EUTHERIA;
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               PIR; A01941; KVMSX4.
HSSP; P01679; 2FBJ.
IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A01941; KVMSX4.
; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYNGDTNYNQKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCAR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYNGGTGYNQKFKSKATLTVDNSSSTAYMELSSLTSEDSAVYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                 FSGSGSGTSYSLTISSMEAEDAAIYYCQQWNYPLITFGGGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNMHWVKQSHGKSLEWIGYIY
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                                                                                                                                                                                      RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107
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24
49
56
88
97
                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 REGION.
23
33
48
55
87
106
106
                                                                                                                                                                                                   CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.18;
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                                                                                                                                                                                                                                      SEQUENCE UP ANNOTATION (XRPC 44).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 420; DB
Pred. No. 2.6e
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAMEWORK 3.

COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING
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BY SIMILARITY.
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TISSUE-INTESTINE;
FISCHER M., KUEPPERS
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HOMO SAPIENS (HUMAN).
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LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 181; DB 2;
Pred. No. 9.1e-07;
3; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 182.5; DB 2
Pred. No. 7.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intestinal plasma cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carry heavily
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Best Local (
               043234 PRELIMINARY; PRT; Y/ AA. 043234; O1-JUN-1998 (TREMBLREL. 06, CREATED) O1-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UP O1-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION RHEUMATOID FACTOR RF-ET13 (FRAGMENT).
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075729;
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01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. TISSUE-INTESTINE;
                                                                                                                                                                                                                                                                                           mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; AJ009526; E1311452; -.
                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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            OMOH
                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                       FISCHER M., KUEPPERS R.; "Human IgA and IgM secreting
                                                                                                                                                                                                                                                                                                                                                                            PRIMATES; CATARRHINI;
                                                                                                                                                                                                                                                                                                                                             FISSUE-INTESTINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 WVKQSHGKNLEWIGLINPYNGDTNYNQKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYY 215
                                                                                                                                               212
                                                                                                                                                                                      152
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            SAPIENS
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                                                                                                                           AVYYCVKDGVSANSVWD-YFDYW
                                                                                                                                               AVYYC----ARRVTDWYFDVW
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78 AA;
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nilarity 42.2%;
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             (HUMAN)
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 CHORDATA;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                           82
                                                                                                                                                                                                         Score 176.5; DB Pred. No. 2e-06; 6; Mismatches
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  VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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Best Local
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                    O75724 PRELIMINARY;
O75724;
O1-NOV-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
11-NOV-1998 (TREMBLREL. 0
1G HEAVY CHAIN VARIABLE R)
VH
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075726;
01-NOV-1998
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NON_TER
SEQUENCE
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                "Human IgA and IgM secreting intestinal plasma cells mutated VH region genes.";
SUBMLITED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS EMBL: AJ009523; E1311446; -.
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01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
IG HEAVY CHAIN VARIABLE
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 HOMO SAPIENS (HUMAN) EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                      HOMO
                                                                                                                                                                                                                                                                                                                                          FISCHER M., KUEPPERS R.;
                                                                                                                                                                                                                                                                                                                                                                                  PRIMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 LQESGPEVVKPGGSMKISCKTSGYSFTGHTM--NWVKQSHCKNLEWIGLINPYNGDTNYN 181
                                                                                                                                                                                      154 MNWVKQSHGKNLEWIGLINPYNGDTNYNQKFKGKATFTVDKSSSTAYMELLSLTSEDSAV 213
                                                                                                                                                                                                                                                                                                                                                              EQUENCE FROM N.A.
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                                                                                                                                                      214 YYCARRVIDWYFDVW 228
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                                                                                                                                                                                                                                                                                                                                                                                           SAPIENS (HUMAN).
RYOTA; METAZOA; CHORDATA;
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                                                                                                                                    YYCVRDSYDRGFDFW
                                                                                                                                                                          LTWVRQAPGKGLEWVATINEDGGEKYYVDSVKGRFTISRDDATNSLYLQMNSLRAEDTAV
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10748
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  CHORDATA;
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                                       08, CREATED)
08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE
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                               REGION (FRAGMENT).
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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Pred. No. 2.9e
23; Mismatches
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  VERTEBRATA; MAMMALIA;
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2.9e-06;
28;
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  EUTHERIA;
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075728
075728;
075728;
1 01-NOV-1998 (TREMBLREL. 08,
1 01-NOV-1998 (TREMBLREL. 08,
01-NOV-1998 (TREMBLREL. 08,
1 01-NOV-1998 (TREMBLREL. RF
                                                                                                                                                                                 Query Match
Best Local S
Matches 29
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Best Local Similarity 50.8%;
Matches 32; Conservative 1
         075721
075721;
01-NOV-1998
01-NOV-1998
01-NOV-1998
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                             FISCHER M., KUEPPERS R.;
"Human 19A and 19M secreting intestinal mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDE EMBL; AJ009525; E1311450; ...
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 į
                                                                                                                                                                                                                                                                                                                                                      HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FISCHER M.,
                                                                                                                                                                                                                                                                                                                TISSUE-INTESTINE;
                                                                                                                                                                                                                                                                                                                                               PRIMATES; CATARRHINI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                       AVYYCARRVIDWYFDVW
                                                                                                                                                            HTMNWVKQSHGKNLEWIGLINPYNGDTNYNQKFKGKATFTVDKSSSTAYMELLSLTSEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WIRQPPGKGLEWIGFIY-YSGNTNYNPSLKSRLTISVDTSKNQFSLKLTSMTAADTAVYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WVKQSHGKNLEWIGLINPYNGDTNYNQKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYY 215
                                                                                                    ALYYCARGKRSEGFDYW
                                                                                                                                         YVMNWIRQAPGEGLQWVSTVTENGG
                                                                                                                                                                                           Similarity
  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATARRHINI;
 3 (TREMBLREL.
3 (TREMBLREL.
3 (TREMBLREL.
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                                                                                                                                                                                 Conservative
                                                   PRELIMINARY
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                                                                                                                                                                                                                                                                                                                                               HOMINIDAE;
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. 08, LAST SEQUENCE UPD
. 08, LAST ANNOTATION U
E REGION (FRAGMENT).
                                                                                                    77
                                                                                                                       228
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08, CREATED)
08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   b; Score 173.5;b; Pred. No. 3.5e12; Mismatches
                                                                                                                                                                                 18;
                                                                                                                                                                               Score 170; DB
Pred. No. 5.6e
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intestinal plasma cells carry heavily
                                                                                                                                                                                                                                   EA14CFDF CRC32;
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                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                          VTFYPDSVKGRFSISRDNSRNTLYLQMNSLRAEDT
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                                                                                                                                                                                                                                                                                             plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; DB 2;
                                                                                                                                                                                          DB 2;
.6e-06;
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AC 07
DT 01
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075742;
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27 01-NOV-1998 (TREMBLREL 08,
27 01-NOV-1998 (TREMBLREL 08,
27 01-NOV-1998 (TREMBLREL RF
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Best Local S
Matches 32
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Best Local S
Matches 31
075727
075727;
01-NOV-1998
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                               "Human IgA and IgM secreting intestinal pl mutated VH region genes."; SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ EMBL; AJ009542; E1311480; -. NON_TER 1 1 NON_TER 76 76 SEQUENCE 76 AA; 8887 MW; 24B28E30 CRC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=INTESTINE;
FISCHER M., KUEPPERS R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FISCHER M., KUEPPERS R.;
"Human IGA and IGM secreting intestinal plasma cells mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS EMBL; AJ009518; E1311436; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; C. PRIMATES; CATARRHINI; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO
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TISSUE-INTESTINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIMATES; CATARRHINI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 MNWVKQSHGKNLEWIGLINPYNGDTNYNQKFKGKATFTVDKSSSTAYMELLSLTSEDSAV 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 AVYYCARRVIDW---YFDVW
                                                                                                                                                                                            214 YYCARRVTDWYFDVW
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RYOTA; METAZOA; CHORDATA; VERTEBRATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                       YFCAKR-DGFYYDYW
                                                                                                                                                                                                                                       MFWVRQAPGKGLEWVALSERDDESTSYADSVKGRFTVSRDISKSTLYLQMSSLRVDDTAV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVYYCARDLMIYPTEYFQDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSMNWVRQAPGKGLEWVSLIGTTDRATFYASSVRGRFTISRDDAKNSLYLQMTSLRDDDT
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                                                                                                                                                                                                                                                                                                                           Conservative
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                                              PRELIMINARY;
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                                                                                                                                                    76
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. 08, LAST SEQUENCE UI
. 08, LAST ANNOTATION
.E REGION (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                         Score 168.5; DB
Pred. No. 7e-06;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 169.5; DB 2;
Pred. No. 6.4e-06;
9; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             intestinal plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ED58A5B2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERTEBRATA; AE; HOMO.
                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC32;
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                                                                                                                                                                                                                                                                                                                         26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             carry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heavily
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                                                                                                                                                                                                                                                                                                                      Gaps
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(TREMBLREL. 08,

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Job time:

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                                                                                                     Query Match
Best Local Similarity
Matches 34; Conserv
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Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                   NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                             O75741 PRELIMINARY; PRT; 77 AA.
075741;
01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *FISCHER M., KUEPPERS R.;

*Human IgA and IgM secreting intestinal plasma cells carry heavily mutated VH region genes.";

SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.

EMBL; AJ009524; E1311448; -.

NON_TER 1 1

NON_TER 1 1

NON_TER 80 80

80 AA; 9351 MW; 63DE158A CRC32;
                                                                                                                                                                                                       "Human IgA and IgM secreting intestinal plasma cells carry heavily mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ009540; E1311476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
VH.
                                                                                                                                                                                                                                                                                                  YG.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       TISSUE-INTESTINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-INTESTINE;
                                                                                                                                                                                                                                                             FISCHER M., KUEPPERS R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 YYCARRVIDWY-FDVW 228
                                                                154 MNWVKQSHGKNLEWIGLINPYNGDTNYNQKFKGKATFTVDKSSSTAVMELLSLTSEDSAV 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 DSAVYYCAR--RVTDWYFDVW 228
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  62
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                                                   MSWVRQAPGKGLEWVSGISGSGDYTYYADSVKGRFTISRDNSKNTLSLQLNSVTAEDTAV 61
YYCARHYYDSSPFDYW 77
                                                                                                                                                                      77
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                      8734 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.3%;
                                                                                                   13.1%; score 165.5; DB 2;
44.7%; Pred. No. 1.2e-05;
tive 13; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 168; DB 2;
Pred. No. 8.1e-06;
6; Mismatches 22;
                                                                                                                                                                    1F7F9E8E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 80;
                                                                                                   Indels
                                                                                                                             Length
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Search completed: May 13, 1999, 10:05:19

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Humanised CDR Mus musculus

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd
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Š protein protein search, using sw model

May 13, 1999, 09:37:42; Search time 23.53 Seconds (without alignments) 203.715 Million cell updates/sec

Run

Title: Perfect score: Sequence:

US-08-704-178-3
1267
1 MDLQLTQSPAILSASPGEKV.....RRVTDWYFDVWGAGTTVTVS 237

Scoring table: BLOSUM62

Searched: 162890 seqs, 20225328 residues

Database : A_Geneseq_34:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

44449876544321 424409876544321	Result No.
	Score
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Single chase Single chase Sequence o Anti-ppl30 Fv(GP-2) i Requence o Anti-human 26-10 sFv. Hunti-funct 18-2-3/TRY Single chase Sequence o CC49/212 Sequence o CC49/212 SPLAP Sequence o Single chase IR-2-3/TRY Chimeric r Single chase	crip
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Query Match 100.0%; Score 1267; DB 1; Best Local Similarity 100.0%; Pred. No. 3.4e-80; Matches 237; Conservative 0; Mismatches 0;

Length 237;

0;

Gaps

0;

RFSGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIKGSTSGSGKSSEGK 120 RFSGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIKGSTSGSGKSSEGK 120

RESULT
W15185
ID W1
AC W1
DT 05
DE S1
KW S1
KW br W15185 standard; Protein; 237 AA.
W15185;
W25185;
W35-JUN-1997 (first entry)
Single-chain anti-erbB2 antibody e23(Fv).
Single chain antibody; variable region; light chain; heavy chain; breast cancer; ovarian cancer; non-small cell lung carcinoma; 181 NQKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCARRVTDWYFDVWGAGTTVTVS 237 181 NQKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCARRVTDWYFDVWGAGTTVTVS 237

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07-OCT-1991; 772270.
07-OCT-1991; US-772270.
07-OCT-1991; US-906555.
30-JUN-1992; US-906555.
14-MAY-1993; US-061092.
(ARON-) ARONEX PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a claimed single-chain antibody, designated e33(FV), which binds to erbB-2. Monoclonal antibody e23 was generated by immunising mice with N/erbB-2 cells overexpressing the gpl85 protein, removing spleen cells and producing hybridomas by standard techniques. Messenger RNA coding for the anti-erbB-2 monoclonal antibody was isolated and converted to cDNA. Regions coding for the heavy- and light- chain variable regions were then amplified by PCR and joined via a sequence encoding a peptide linker. The resulting single-chain antibody is useful for in vitro diagnosis of tumour cells which overexpress the erbB-2 gpl85 marker, e.g. breast, ovarian and non-small cell lung carcinomas, and, when coupled to a cytotoxic agent, to treat such tumours. Sequence 237 AA;
             (MOLE-) MOLECULAR ONCOLOGY Kasprzyk PG, King CR; WPI; 94-025878/03.
                                                                                                                                              21-JUL-1994 (first entry)
Sequence of the single chain anti-erbB2 antibody, Ab no.23
Single chain anti-erbB1 antibody; cancer therapy; prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bird RE, Kasprzyk PG, WPI; 97-064831/06. N-PSDB; T65006.
                                                         06-JAN-1994.
21-OCT-1992; U08545.
30-JUN-1992; US-906555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cells expressing this protein Claim 2; Columns 25-28; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single chain antibodies specific for erbB-2 labels or cytotoxin, useful for detection ar
                                                                                                                    Synthetic.
                                                                                                                                   monoclonal antibody
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llarity 100.0%;
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Pred. No. 3.4e-80;
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The source of human erbB-2 protein for the prodn. of antibodies not and 21 (055180/R45442; 055181/R45443) is a NIH/3T3 cell 23 and 21 (055180/R45442; 055181/R45443) is a NIH/3T3 cell engineered to express the human erbB-2 protein on its surface (N/erbB-2). Abs no. 21 and 23 are directed against the extracellular domain of gpl85 erbB-2. Nude mice manipulated to produce rapidly growing tumours were used in a trial of the efficacy of the Abs. I animals given a combination of the 2 Abs, tumours completely regressed after 11 days.
                                             soluble fraction by co-expression with chaperonin. Using the methods scFv can be produced in E. coli, either in a soluble fraction or in inclusion bodies. Like the parent double chain antibodies, the scFv polypeptides are useful in immunological diagnosis or for separation and purification, but they lessen the side effects caused by antibody constant regions. The availability of scFv polypeptides contributes to fundamental research and development of diagnostic and therapeutic
                                                                                                                                                                                                                               Producing single chain Fv antibody in Escherichia coli - by expression in an inclusion body, followed by protein folding or by co-expression with a chaperonin as a soluble fraction Claim 4; Page 6-7; 9pp; Japanese.

The sequences given in W25783-84 represent single chain Fv (scFv) antibodies which are produced in E.coli. The scFv's are derived from an anti-T3 antibody or an anti-T9130 antibody and are produced either by: (1) expression as an inclusion body, followed by folding (1.e. by denaturation and solubilisation) or (2) expression as an entity of the method of the protein by converges on the protein with chaperonia Instant the method of the protein by converges on the protein with chaperonia Instant the method of the protein by converges on the protein with the protein the method of the protein the protein with the protein the method of the protein the protein with the protein the protein the protein with the protein the pr
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JP-027622.
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Matches
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MAD capable of binding to the gamma chain of the IL-2 recept thus of blocking the IL-2 response, is produced by mouse hyb line GP-2 (FERM BP-4641). DNA encoding the variable region this MAD was expressed in E. coli, yielding Fv(GP-2) with immunosuppressive activity.
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MAb; monoclonal antibody; hybridoma; interleukin-2;
Fv; antibody variable region; GP-2; Fv(GP-2);
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07-MAR-1994; JP-036065.
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Matches 162
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Example 1; Fig 11 and Page 29-31; 50pp; English.

The VL and VH sequences of the anti-CD3 hybridoma G19-4 were amplified by PCR methods. A gene fusion was constructed from the two amplified domains and a (G1948er)3 linker. The amino terminus of the VL-VH fusion cassette was fused at the SalI site to the L6 light chain variable region leader peptide and the carboxy-terminus was fused directly to the hinge region of the Fc domain at the BcII site and/or to a short "helical" peptide linker to construct the bispecific CD3-L6FvIg antibody derivative. The variable regions for L6 were fused in frame to the opposite end of the helical linker (not included in R60206).
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31 JAN-1994; 300692.
01 FEB-1993; US-013420.
13-SEP-1993; US-121054.
(BRIM ) BRISTOL-MYERS SQUIBB CO.
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10-AUG-1994.
31-JAN-1994;
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Linsley PS;
WPI; 94-250885/31.
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helical peptide linker; anti-L6 antibody; tumour cell antigen;
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.8e-51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I labels or cytotoxin, useful for detection and treatment of tumour process of claim 2; Columns 27-30; 288p; English.

Claim 2; Columns 27-30; 288p; English.

The present sequence represents a claimed single-chain antibody, 20 designated e21(FV), which binds to erbB-2. Monoclonal antibody e21

Cwas generated by immunising mice with N/erbB-2 cells overexpressing the gp185 protein, removing spleen cells and producing hybridomas 20 cmonoclonal antibody was isolated and converted to cDNA. Regions 20 coding for the heavy- and light- chain variable regions were then 21 coding for the heavy- and light- chain variable regions were then 21 coding for the heavy- and light- chain variable regions were then 22 coding for the heavy- and light- chain variable regions were then 22 coding for the heavy- and light- chain variable regions were then 23 coding for the heavy- and light- chain variable regions were then 24 coding for the heavy- and light- chain antibody is useful for in vitro 25 coding for the process the resulting single-chain antibody is useful for in vitro 27 cd diagnosis of tumour cells which overexpress the erbB-2 gp185 cm arker, e.g. breast, ovarian and non-small cell lung carcinomas, 25 cm 23 paa;
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Best Local
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07-OCT-1991; 772270.
07-OCT-1991; US-772270.
07-OCT-1991; US-772270.
30-JUN-1992; US-906555.
14-MAY-1993; US-061092.
(ARON-) ARONEX PHARM INC.
Bird RE, Kasprzyk PG, Ki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus
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Single chain antibody; variable region; light chain; heavy chain; breast cancer; ovarian cancer; non-small cell lung carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W15186 standard; Protein; W15186;
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                                                                                                                                                                                           KFQGKASITADTSSNAAYLQLSSLTSEDTAVYYCA---SYYYYSAYYAMYYWGQGTSVTV
                                                                                                                                                                                                                                                                                                                                                                                    SGSGSGNSYSLTISSMEAEDAATYYCYQGSGYPFTFGSGTKLEIKGSTSGSGKSSEGKGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ific for erbB-2 protein, for detection and treatme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 795.5; DB:
Pred. No. 6.9e-48,
2; Mismatches 49
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RESULT
R60781
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EP-621338-A.

26-0CT-1994; 106257.

F 21-APR-1994; 106257.

PR 21-APR-1994; JP-094491.

PR 07-MAR-1994; JP-036055.

PR 07-MAR-1994; JP-036055.
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Best Local Similarity
Matches 155; Conser
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R45443;
21-JUL-1994
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Example; Fig 8; 37pp; English.

The source of human erbB-2 protein for the prodn. of antibodies in the source of human erbB-2 protein on its surface (Note 1) and 21 (Q55180/R45442; Q55181/R45443) is a NIH/3T3 cell engineered to express the human erbB-2 protein on its surface (Note 1) and 23 are directed against the extracellular domain of gp185 erbB-2. Nude mice manipulated to produce rapidly growing tumours were used in a trial of the efficacy of the Abs.

The surface after 11 days.
                                                                                                                                                                                                       Fv(GP-4) immunosuppressive.
MAb; monoclonal antibody; hybridoma; interleukin-2;
Fv; antibody variable region; GP-4; Fv(GP-4);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JAN-1994.
21-OCT-1992; U08545.
30-JUN-1992; US-906555
                            WPI; 94-325948/41.
N-PSDB; Q73679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treatment of malignancies over 2 monoclonal antibodies which
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WPI; 94-025878/03.
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Immunosuppressant polypeptide interleukin-2 response
                                                          Hamura J, K
Takeshita T;
                                                                                                                                                                                             immunosuppressive.
                                                                                                                                                                                                                                                         09-MAY-1995
                                                                                                                                                                                                                                                                                       R60781 standard;
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gle chain anti-erbB2 antibody, Ab no.21.
rbB1 antibody; cancer therapy; prevention;
                                                                                                                                                                                                                                                            entry)
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                                                                        Nakazawa
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hich recognise different e
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No. 9.5
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PT the serpin enzyme complex receptor, used in gene therapy of the serpin enzyme complex receptor, used in gene therapy of the serpin enzyme series an anti-human SC single chain Fv/protamine fusion protein Sequence containing a target binding molety capable of binding molety. CC This can be used in a method for delivering an oligonucleotide to a commandian cell. The method comprises conjugating the target binding cc mammalian cell. The method comprises conjugating the target binding cc the carrier to an expression vector encoding one or more gene products to form a pharmaceutical composition. A mammalian cell having on its confacted with the pharmaceutical composition under conditions allowing binding to the receptor resulting in delivery of the charmaceutical composition to the introduction of exogenous genetic material composition are used for the introduction of exogenous genetic material composed a functional wild-type or mutant gene or may be an antisense sequence or other nucleic acid having a therapeutic effect. The fusion cc protein may comprise a protein portion having therapeutic properties, cc e.g. enzymatic activity, cytokine activity and antibiotic activity which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Ma
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Matches
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MAb capable
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(UYCA-) UNIV CASE WESTERN RESERVE.
                                                                                                                                                                                                                                                                                                                                                                                 WO9746100-A1.
11-DEC-1997.
03-JUN-1997; U09858
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-human SC single chain Fv/protamine fusion protein. Fusion protein; SC single chain Fv/protamine fusion protein; SECR; exogenous gene; serpin enzyme complex receptor; gene therapy; target binding moiety.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W37085
                                                                                                                                                                                                                                                                                         Delivering compacted exogenous nucleic acid to cells
                                                                                                                                                                                                                                                                                                           N-PSDB; V00611.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  m 9; Page 27-28; 37pp; English.

capable of binding to the gamma chain of the IL-2 recept
of blocking the IL-2 response, is produced by mouse byt
GP-4 (FERM BP-4640). DNA encoding the variable region
MAD was expressed in E. coli, yielding Fv(GP-4) with
                                                                                                                                                                                                                                                                                                                      98-041783/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STQVKLEESGPELVKPGASVKISCKASGYSFTGYYMHWVKQSHVKSLEWIGRINPYNGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKGVQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGLINPYNGDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MDLQLTQSPAILSASPGEKVTMTCRATPSV-SYMHWYQQKPGSSPKPWIYTTSNLASGVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MDILLTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNAKTLADGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
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63.5%;
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Pred.
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                                                                                                                                                                                                                                                                                         targeting
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R34672
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Best Local S
Matches 156
                                                                                                                                                                                    16-OCT-1992; UO8881.
18-OCT-1991; US-777709.
(UYCA-) UNIV CALGARY.
Anthony JG, Mg SC, Wo
WPI; 93-152491/18.
N-PSDB; Q41069.
Expression-secretion vectors - for prodn. of biologically active antibody Fv fragments or single chain Fv molecules Disclosure; Fig 6; Slpp; English.

This sequence represents a single chain Fv molecule which contains the heavy and light variable portions (VH and VL) of antidigitoxin monoclonal antibody (MAb) 26-10 (see also R34670-71), a signal sequence (see R38527-28) and a linker between the two variable regions. The DNA sequence encoding this protein was used in the construction of an expression-secretion system for the production of biologically active Fv fragments. The system also contains a DNA sequence encoding the T7 promoter. The secretion-expression vector was produced by polymerase chain reaction Fv fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is delivered to a cell surface via the SECR binding moiety. The nucleic acid can be compacted at high concentrations with the carrier molecule a critical salt concentration. The condensation of such complexes provides structural features to the DNA/cationic lipid complex that prolong in vivo expression.

Sequence 301 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression-secretion system;
polymerase chain reaction; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-10 SFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heavy; light; vantibody; MAb;
                                                                                                                                                                                                                                                                               WO9308300-A.
29-APR-1993.
                                                                                                                                                                                                                                                                                                                                                        peptide
                                                                                                                                                                                                                                                                                                                                                                                     region
                                                                                                                                                                                                                                                                                                                                                                                                                   peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSSEGKGVQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGLINPY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGVPARFSGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIK-GSTSGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WGQGTTLTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WGAGTTVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGGTSYNQKFKGKATLTVDKSSTTAYMELRGLTSEDSAVYSCAR----YYRYDVLSAMDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGDTNYNQKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCARRVTDWY-----FDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSGGGSEVQLQQSGPDLVKPGASVKISCKTSGYTFIEYTMHWVKQSHGKSLEWIGGINPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGVPGRFSGSGSGTDFSLNIHPMEEDDTAMYFCQQSKAVPYTFGGGTKLEIKGGGGSGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MDIVLTQSPASLAVSLGQRATISCRASESVDNYAISFMNWFQQKPGQPPKLLIYAASNQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            light; variable; VH; VL; region; antidigitoxin; monoclonal; dy; MAb; 26-10; Fv; fragment; antigen; binding site; linker; sion-secretion system; T7 promoter; signal peptide; molecule rase chain reaction; PCR; single chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                U08881.
US-777709.
                                                                                                                                                                                                                                                                                                                                                         /note-
139. .:
                                                                                                                                                                                                                                                                                                                          /label=
154. .27
                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                             /note-
                                                                                                                                                                                                                                                                                                                                                                                       .138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                    Wong
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62.4%;
                                                                                                                                                                                                                                                                                                                                                         .153
                                                                                                                                                                                                                                                                                                                                                                      "26-10 VL sequence"
                                                                                                                                                                                                                                                                                                            "26-10 VH sequence"
                                                                                                                                                                                                                                                                                                                                         Linker peptide
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Pred.
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No. 6.
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.9e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               molecule,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                      The multifunctional protein comprises a single chain biosynthetic Ab binding site (comprising sequences minicking the light chain and heavy chain variable regions of murine monoclonal 26-10) with the specificity of murine monoclonal 26-10, linked through a spacer to the FB fragment of protein A, here fused as a leader, and constituting a binding site for FC protein A, here fused as a leader, and constituting a binding site for FC protein A, here fused as a leader, and constituting a binding site for FC protein C adilute acid cleavage site). The construct contains the light spacer contains among acids of the FB followed by Asp-Pro ( a dilute acid cleavage site). The construct contains commarised as: FB-Asp-Pro-VI-(G14-Ser)3-VH. The protein can be used for specific binding assays, affinity purificn. biocatalysts, targetting, imaging an immunological treatment of oncogenic and infectious diseases. It offers fewer cleavage sites to circulating proteolytic enzymes, and comproved stability. It reaches target tissues rapidly and its quickly cleared from the body. It also has reduced immunogenicity and its design facilitates binding to other moieties in drug targetting and imaging
Query Match
Best Local Similarity 58.5
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprising o
be used to s
full length
                                                                                                                                                                                                                                                                                                                                                                                                Recombinant multifunctional protein - having antibody binding sequence for biological activity, ion sequestering or binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1988.
19-MAY-1988; U01737.
21-MAY-1987; US-052800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Multifunctional protein.
Multifunctional protein; biosynthetic
murine monoclonal 26-10.
                                                                                            applications.
Sequence 251
                                                                                                                                                                                                                                                                                                                                                                     Disclosure; 15pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; N80178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CREA-) Creative Biomolecules Huston JS, Oppermann H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Multifunctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-OCT-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P80152 standard; protein; 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 DLQLTQSPAILSASPGEKVTMTCRATPSV-----SYMHWYQQKPGSSPKPWIYTTSNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGVPARFSGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIK--GSTS-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                 88-353928/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYNGDTNYNQKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCA-RRVTDWYFDVWGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLNWYLQKAGQSPKLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYSGVTGYNQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCAGSSGNKWAMDYWGHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGVPDRFSGSGSGTDFTLKISRVEAEDLGIYFCSQTTHVPPTFGGGTKLEIKRGGSGSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       only the VH or VL regions, and single chain molecules specifically bind one or more of the same antigens as h antibody from which they are derived.

272 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237
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                                                                                                                                                                                                                                                                                                                                                                       English
                             58.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
              Score 746; DB
Pred. No. 1.8e
34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 748; DB 1;
Pred. No. 1.4e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody binding site;
                             DB 1;
.8e-44;
                  57;
                                            Length 251
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                12;
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to a
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W02191
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                                                                                                                                                                      Query Match
Best Local S
Matches 144
                                                                                                                                                                  for labelled or immobilised antibody, are less immunogenic, easier to engineer, more stable and less expensive Example 9; Fig 39A-B; 78pp; English.

C Computer-designed construct 18-2-3/TRY202 (W02191), encoded by the DNA sequence given in T36463, comprises the variable regions of the light and heavy chains of anti-fluorescein monoclonal cantibody (Mab) 18-2-3 linked by a peptide designed to fit into a groove on the backside of the variable domain structure. The DNA construct was inserted into vector pGX3703 and introduced into E. coli. 18-2-3/TRY202' was produced as a single chain molecule. It cexhibited biological binding activity equivalent in specifically and affinity to that of the original MAb.
                                                                                                                                                                                                                                                                                                                                                                                                              21-MAY-1996.
02-SEP-1986; US-902971.
02-SEP-1986; US-902971.
02-SEP-1987; US-092110.
19-JAN-1989; US-299617.
25-APR-1999; US-512910.
01-APR-1993; US-468988.
(ENZO-) ENZON LABS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-NOV-1996 (first entry)
18-2-3/TRY202' single chain binding protein.
Antibody engineering; monoclonal antibody; MAb;
single chain antibody; immunoassay; fluorescein; 18-2-3/TRY202';
single chain binding protein.
                                                                                                                                                                                                                                                                                                                                                                        Bird RE, Hardman K,
WPI; 96-259060/26.
N-PSDB; T36463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5518889-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric synthetic
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                                                                                                                                                                                                                                                                                                                                                         Immunoassay using single chain antigen binding
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                                     GGGGSGGGGSEVQLQQSGPELVKPGASVRMSCKSSGYIFTDFYMWWVRQSHGKSLDYIGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INPYNGDTNYNQKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCA-RRVTDWYFDVWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGSGKSSEGKGVQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGVPDRFSGSGSGTDFTLKISRVEAEDLGIXFCSQTTHVPPTFGGGTKLEIKRGSGGGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLNWYLQKAGQSPKLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLQLTQSPAILSASPGEKVTMTCRATPSV-----
PARFSGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIKGSTSGSGKSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTTVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISPYSGVTGYNQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCAGSSGNKWAMDYWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGVPARFSGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIK-----GST
                                                                                               Conservative
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                                                                                            Score 745; DB 1;
Pred. No. 2e-44;
40; Mismatches !
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61

PARFSGGGSGTSYSLTISSVEAEDAATYYCQQYSGYPLTFGAGTKLELEGKSSGSG-

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RASULT PROCESS OF SECOND PROCE
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PI Bird RE, Hardman K, Ladner RC;

DR WPI; 93-367875/46.

DR WPI; 93-367875/46.

DR N-PSDB; 051540.

PT Single chain poly:peptide for binding antigen - comprising light PT and heavy chain antigen binding portions linked by peptide linker PS Example 9; Figure 39; 78pp; English.

CC The single chain polypeptide is derived from the mature light and CC heavy chains of a monoclonal antibody (MAb) and has affinity CC for a given antigen (Fluorescein). It comprises a first CC comprising the antigen binding portion of of the light CC comprising the antibody and a second polypeptide CC comprising the antibody and a second polypeptide CC comprising the antibody and a second polypeptide CC crain variable region of an antibody and a second polypeptide comprising the antipody and at least one peptide linker linking the CC crist and second polypeptide chains. The resulting single chain CC polypeptide can be used in diagnostics, therapy CC (in vivo and in vitro), imaging, purifications and biosensors.

CC This particular single chain binding molecule was designated CC sequence 23 and contains one linker peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Sim
Matches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
US5260203-A.
US5260203-A.
09-NOV-1993.
02-SEP-1986; US-902971.
02-SEP-1987; US-092110.
19-JAN-1989; US-29617.
25-APR-1990; US-512910.
(ENZO-) ENZOM INC.
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Single chain polypeptide with affinity for fluorescein.
Monoclonal antibody; MAb; affinity; binding; antigen; cherapy; imaging; purification; biosensors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R43679
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                                                                                                                                                        PARFSGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIKGSTSGSGKSSE
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                                                      NYNSALMSRLSISKDNSKSQVFLKMNSLQIDDTAIYYCAKRLGRIFYYAMDYWGQGTSVT
                                                                                                       NYNQKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCARRVTDWYF---DVWGAGTTVT
                                                                                                                                                                                                                                                                         PARFSGGGSGTSYSLTISSVEAEDAATYYCQQYSGYPLTFGAGTKLELEGKSSGSG--SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 742; DB
Pred. No. 3.2e
39; Mismatches
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                                                                                                                                                                                                                                                                                                                          Immuno:purifico. using single binding chain molecule including parts of antibody light and heavy chain variable regions connected by a linker - is smaller, stabler and less expensive than complete antibodies

Example 9; Fig 39; 78pp; English.

A DNA construct (713739) codes for single chain binding molecule 18-2-3/TRY202' (R99649), in which VL and VH regions of anti-C increscein monoclonal antibody 18-2-3 are joined by a peptide linker composed primarily of alternating Gly and Ser residues, with C Glu and Lys residues to enhance solubility. The construct was cobtd. which was capable of exhibiting a biological binding activity cobtd. which was capable of exhibiting a biological binding activity antibody. SCAS (see also R99645-48 and T99650-51) have the advantages of smaller size, greater stability and reduced cost.
                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JUL-1996.
02-SEP-1986; US-902971.
02-SEP-1986; US-902971.
02-SEP-1987; US-092110.
19-JAN-1989; US-299617.
25-APR-1990; US-512910.
01-APR-1990; US-512910.
06-JUN-1995; US-468992.
(ENZO-) ENZON LABS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single chain binding molecule 18-2-3/TRY202'.

Antibody engineering; single polypeptide chain binding single chain antibody; SCA; heavy chain; light chain; monoclonal antibody; MAD; immunoaffinity purification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bird RE, Hardman K, WPI; 96-333309/33. N-PSDB; T13739.
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238
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VS
                        ٧S
                                                                                                    GKGVQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGLINPYNGDT
                                                                                                                                                     PARFSGGGSGTSYSLTISSVEAEDAATTYCQQYSGYPLTFGAGTKLELEGKSSGSG--SE
                                                  NYNSALMSRLSISKDNSKSQVFLKMNSLQIDDTAIYYCAKRLGRIFYYAMDYWGQGTSVT
                                                                NYNQKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCARRVTDWYF---DWGGGTTVT
                                                                                                                                                                                 PARFSGGGSGTSYSLTVSRVEAEDAATTYCQQWSRSPPTFGGGSKLEIKGSTSGSGKSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /TRY202'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; Protein; 239 AA.
239
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                                                                                                                                                                                                                                                                           58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ladner
                                                                                                                                                                                                                                                                39;
                                                                                                                                                                                                                                                               Score 742; DB
Pred. No. 3.2e
39; Mismatches
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                                                                                                                                                                                                                                                        DB 1,
3.2e-44;
51;
                                                                                                                                                                                                                                                                                      Length 239;
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Search completed: May 13, 1999, 10:02:41 Job time: 1499 sec

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Copyright (c) 1993 - 1998 Compugen
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ALIGNMENTS

RESULT PC4402

hapten-specific single-chain antibody variable fragment and alkaline phosphatase: C;Species: Escherichia coli
C;Species: O3-Sep-1998 #sequence_revision O3-Sep-1998 #text_change O3-Sep-1998
C;Accession: PC4402
R;Suzuki, C:, Ueda, H.; Suzuki, E.; Nagamune, T.
J. Biochem. 122, 322-329, 1997
A;Title: Construction, bacterial expression, and characterization of hapten-specif A;Reference number: PC4402
A;Reference number: PC4402
A;Recession: PC4402
A;Recression: PC4402
A;Ressidues: 1-287 <SUZ>

bacterial expression, and characterization of hapten-specific

fusi

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Ig heavy chain V region precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text C;Accession: S52445 R;Berdoz, J.; Kraehenbuhl, J.P. submitted to the EMBL Data Library, November 1994 s.Description: Specific amplification by the polymerase A;Description: Specific amplification by the polymerase
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                                                    A; Introns: 16/1
C; Superfamily: immunoglobul.
C; Keywords: heterotetramer;
                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-137 <BER>
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                                                                                                        A;Cross-references: EMBL:X82690; NID:g673439; C;Genetics:
                                                                                                                                                                                             A; Reference number: S52445
A; Accession: S52445
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Best Local Sim
Matches 121;
Query Match
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                                                  immunoglobulin V region; immunoglobulin homology
terotetramer; immunoglobulin
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Score
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3.6e-36;
nes 79;
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Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Feb-1991 #sequence_revision 13-Sep-1991 #text_change 20-Mar-1998
C:Accession: A34871
R:Chaudhary, V.K.; Batra, J.K.; Gallo, M.G.; Willingham, M.C.; FitzGerald, D.J.; Past. Proc. Natl. Acad. Sci. U.S.A. 87, 1066-1070, 1990
A:Tittle: A rapid method of cloning functional variable-region antibody genes in Esche. A; Reference number: A34871; MUID:90138938
A; Reference number: A34871; MUID:90138938
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-120 <CHA>
A; Cross-references: GB.M34000
A; Note: the authors translated the codon TTT for residue 88 as Pro
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                            Ig light chain V region (S107/VH11 group 2-36) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
C;Accession: PT0398
R;Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
J. Exp. Med. 173, 731-741, 1991
A;Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA A;Reference number: PT0376
A;Accession: PT0398
A;Accession: PT0398
A;Accession: PT0398
A;Molecule type: DNA
A;Residues: 1-107 <BEH>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                          PT0398
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86.1%;
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                                                                   Score 496; DB 2;
Pred. No. 2.1e-31;
5; Mismatches 5;
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8
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                                                                                               Length 107
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A; Reference number:
A; Accession: $25058
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Ig kappa chain - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 19 Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Sep-1997
C;Date: 19 Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Sep-1997
C;Accession: S25058
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, submitted to the EMBL Data Library, July 1992
submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop
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A;Accession: PT0402
A;Molecule type: DNA
A;Residues: 1-107 <BEH>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-235 <FIS>
A;Cross-references: EMBL:X67211; NID:g54828; PID:g54829
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                                                         QGKASITADTSSNAAYLQLSSLT-SEDTAVYYCASYYYYSAYYAMYYWGQGTSVTVSSY
                                                                                                                                                                                         QQSGVELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIHPENGNTVYDPKF 182
                                                                                                                                                                                                                                                                                        SGSGNSYSLTISSMEAEDAATYYCYQGSGYPFFTFGSGTKLEIKGSTSGSGKSSEGKGVQL 122
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                                                                                                                             PPSSEQLTSGGASV--VCFLNNFYPKDINVKWKIDGSER
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---NSWTDQDSKDSTYSMSSTLTLTKD-----EYERHNSYTCEATHKTSTSPIVKSF
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Pred. No. 4.3e-31;
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C;Accession: S049/0
R;Kofler, R; Noonan, D.J.; Strohal, R.; Balderas,
Eur. J. Immunol. 17, 91-95, 1987
Eur. J. Immunol. 17, 191-96 of the murine lupus-as:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL;X14624; NID:g52029; PID:g52030 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;T-19/Domain: signal sequence #status predicted <SIG> F;1-19/Pomain: signal sequence #status predicted +STG> F;20-136/Product: Ig heavy chain V region (fragment) #status predicted
Ig light chain V region (S107/VH11 group 2-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
                                                             RESULT
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A;Residues: 1-107 <BEH>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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A; Residues: 1-136 < KOF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: PT0403
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;Species: Mus musculus (house mouse)
;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 3
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Species: Mus musculus (house mouse)
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                                                                                                                                                             SGSGNSYSLTISSMEAEDAATYYCYQGSGYPETFGSGTKLEIK 105
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                                                                                                                                                                                                                        LTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSSTSPKLWICDTSKLASGVPGRFSG 63
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Pred. No. 1.2e-30;
6; Mismatches 17
                                                                                                                                                                                                                                                                                                                         Score 486; DB 2;
Pred. No. 1.2e-30;
                                                                                                                                                                                                                                                                                                          Mismatches
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30-Sep-1993 #text_change 30-Sep-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S.; Scharff,
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                                                                                                                                                                                                                                                                                                                                            Length 107
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                                                                                                                                                                                                                                                                                                      0;
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A; Molecule type: DNA
A; Residues: 1-107 <BEH>
C; Superfamily: immunoglobulin V region;
C; Keywords: immunoglobulin
                                                                                                                               R:Jarrin, A.; Andrieux, A.; Chapel, A.; Buchou, T.; Marguerie, G
FEBS Lett. 354, 169-172, 1994
A:Title: A synthetic peptide with anti-platelet activity derived
A:Reference number: S51210
A:Accession: S51210
                                                                                                                                                                                                                             Ig kappa chain V region (AC7) - mouse C;Species: Mus musculus (house mouse) C;Date: 01-Aug-1995 #sequence_revision C;Accession: S51210; S58928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-107 <BEH>
C;Superfamily: immunoglobulin V
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig light chain V region (S107/VH11 group 2-2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantib A; Reference number: PT0376 A; Accession: PT0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: PT0400
R;Behar, S.M.; Lustgarten, D.L.; Corbet,
J. Exp. Med. 173, 731-741, 1991
                                     A; Molecule type: protein A; Residues: 1-20 < JAR2>
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A;Accession: PT0401
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                                                                                             A; Molecule type: mRNA
A; Residues: 9-99 < JAR>
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                                                                             A; Accession: S58928
Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin
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Best Local
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Pred. No. 2.5e-30;
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Pred. No. 2.5e-30;
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A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four an hypervariable regions.

A;Reference number: $03471; MUID:84057768

A;Reference number: $03471; MUID:84057768

A;Recession: $03471

A;Molecule type: mRNA

A;Residues: 7-120 <ROC1>
A;Residues: 7-120 <ROC1>
A;Cross-references: EMBL:X01820; NID:g51833; PID:e29256; PID:g133983

A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Immunol. 129, 2554-2558, 1982

A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does
A;Reference number: 807453; MUID:83058021

A;Recession: $07453

A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Keywords: heterotetramer; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_ci
C;Accession: PT0397
R;Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
J. Exp. Med. 173, 731-741, 1991
A;Title: Characterization of somatically mutated S107 VH11
A;Reference number: PT0376
A;Accession: PT0397
                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment) C;Speciles: Mus musculus (house mouse) C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Sep-1997 C;Accession: S03471; S07453
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A;Residues: 1-107 <BEH>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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EMBO J. 2, 867-872,
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Best Local S
Matches 89
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;Species: Mus musculus (house mouse)
;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
;Accession: PT0397
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Best Local Similarity
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sh 37.8%; Similarity 86.4%; 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                  .; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau,
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Pred. No. 3.5e-30;
7; Mismatches 7;
 Score 475;
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 Length
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Best Local Sin
Matches 88;
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                  QGTSVTVSS
                  239
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C;Accession: S29594
R;Seymour, R.
submitted to the EMBL Data L
A;Reference number: S29593
A;Accession: S29594
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
pr0395
Ig light chain V region (S107/VH11 group 2-16) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 3
C;Accession: pr0395
C;Accession: pr0395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig gamma chain (WM65) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-107 <BEH>
C;Superfamily: immunoglobulin V region; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantib A; Reference number: PT0376 A; Accession: PT0395
                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X57857; NID:g52590; C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: immunoglobulin C; Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Behar, S.M.; Lustgarten, D.L.; Corbet, J. Exp. Med. 173, 731-741, 1991
                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-178 <SEY>
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                                                                                                     111 SGKSSEGKGVQLQQSGVELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIH 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 VQLQQSGVELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIHPENGNTVYD 179
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                   PENGNTVYDPKFQGKASITADTSSNAAYLQLSSLTSEDTAVYYCASYYYYSAYYAMYYWG 230
                                                                               PANGYTEYDPKFQGKATITADTSTNTAYLQLSSLTSEDTAVYYCTGGNY---AYGMDYWG
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                                                                                                                                                                  . Similarity
96; Conserv
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88; Conservative
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Pred. No. 3.5e-29;
"""matches 20; Indels
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Pred. No. 1e-29;
7; Mismatches
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4; Mismatches 18;
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Search completed: May 13, 1999, 10:03:48 Job time: 1380 sec

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Мау 13, 1999, 10:05:48 ; Search time 16.53 Seconds (without alignments) 389.696 Million cell updates/sec

Run

Perfect score: US-08-704-178-4 1271

Sequence: MQLTQSPAIMSASPGEKVTM......SAYYAMYYWGQGTSVTVSSY 240

Scoring table: BLOSUM62

Searched: 74019 seqs, 26840295 residues

Database : SwissProt_36:*

and is No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

SUMMARIES

Result

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> 3 LTQSPAIMSASPGEKVTMTCSASSSVSNMHWYQQKSSTSPKLWVYDTSKLASGVPGRFSG 62

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64 63

SGSATSYSLTITSMQAEDAATYYCQQWSSNPLTFGAGTKLELK 106 SGSGNSYSLTISSMEAEDAATYYCYQGSGYPFTFGSGTKLEIK 105

RESULT TO THE STATE OF THE STAT Query Match Best Local S Matches 86 P04940;
13-AUG-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
1G KAPPA CHAIN V-VI REGION (NQ2-17.4.1).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TET TLT 1 MOUSE KV6F_MOUSE DISULFID NON_TER SEQUENCE DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN MEDLINE; 83271467.

KAARTINEN M., GRIFFITHS G.M., MARKHAM A.F.,

NATURE 304:320-324(1983).

-!- EUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX)

EMBL; K00735; G196435; -.

HSSP; P01679; 1FVB. DOMAIN DOMAIN SEQUENCE FROM N.A. IMMUNOGLOBULIN V REGION; 86; Similarity Conservative 24 49 56 88 97 STANDARD; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; 11561 MW; 35.4%; HYBRIDOMA. 6; Score 450; DB 1; Pred. No. 2.1e-28; 6; Mismatches 11 COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
BY SIMILARITY. FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING FRAMEWORK 3. COMPLEMENTARITY-DETERMINING FRAMEWORK 1. PRT; 1BC0C1E3 CRC32; ALIGNMENTS 107 (PHOX) ANTIBODY À MILSTEIN C.; Length 107; Indels 2 0, Gaps 0

THE REAL PROPERTY OF THE PROPE NGJ_MOUSE STANDARD; PRT; 107 AA.

P04944;
P04944;
11-AUG-1987 (REL. 05, CREATED)
11-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
101-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
101-CT-1993 (REL. 27, LAST ANNOTATION UPDATE)
101-CT-1987 (REL. 20, CHORDATA; VERTEBRATA; TET)
102-CT-1987 (REL. 20, CHORDATA; VERTEBRATA; TET)
103-CT-1987 (REL. 20, CHORDATA; VERTEBRATA; TET) SEQUENCE FROM N.A.

MEDLINE: 83271467.

KAARTINEN M., GRIFFITHS G.M., MARKHAM
KAARTINEN M., GRIFFITHS G.M., MARKHAM
NATURE 304:320-324(1983).

1- FUNCTION: ANTI-2-PHENYL OXAZOLONE
EMBL; K00744; G194453; -.

HSSP; P01679; 1FVB. DOMAIN EUTHERIA; RODENTIA. IMMUNOGLOBULIN V REGION; HYBRIDOMA DOMAIN 1 23 FRAMEN CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; FRAMEWORK 1. (PHOX) ANTIBODY. A.F., UPDATE) A A

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RESULT 4
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IQ KV6G_MOUSE
AC P04941;
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Best Local :
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MEDLINE; 83271467.

KAARTINEN M., GRIFFITHS G.M., MARKHAM A.

NATURE 304:320-324(1983).

-!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (P.

EMBL; K00740; G196445;

HSSP; P01679; 1FVB.

IMMUNOGLOBULIN V REGION; HYBRIDOMA.
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P04943;
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13-AUG-1987
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-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
-CCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
KAPPA CHAIN V-VI REGION (NQ6-8.3.1).
SMUSCULUS (MOUSE).
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i; Mismatches
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Pred. No. 5.
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
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COMPLEMENTARITY-DETERMINING
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Pred. No. 4.3e-28
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.

BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING
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COMPLEMENTARITY-DETERMINING
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RESULT 5
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Best Local (
                                                                                                                                                                                                                                                                                                                                                        KV6H_MOUSE STANDARD; PRT; 107 AA.

P04942;

P04942;

13-AUG-1987 (REL. 05, CREATED)

13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)

10-CCT-1993 (REL. 27, LAST ANNOTATION UPDATE)

1G KAPPA CHAIN V-VI REGION (NQ5-61.1.2).

MUS MUSCULUS (MOUSE).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAI

EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

REDLINE; 83271467.

KAARTINEN M., GRIFFITHS G.M.,

NATURE 304:320-324(1983).

-!- FUNCTION: ANTI-2-PHENYL OJ

EMBL; K00737; G196439; -

HSSP; P01679; 1FVB.

IMMUNOGLOBULIN V REGION; HYBR.
DOMAIN
DISULFID
NON_TER
SEQUENCE
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NON_TER
SEQUENCE
                                                                           DOMAIN
DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                             -!- FUNCTION: ANTI-2-PHENYL EMBL; K00739; G196443; -. HSSP; P01679; 1FVB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
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13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN V-VI REGION (NO2-48.2.2).
MUS MUSCULUS (MOUSE).
EUKREYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                    NATURE 304:320-324(1983
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 83271467.
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                                                                                                                                                                         DOMAIN
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                                                                                                                                                                                             IMMUNOGLOBULIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTQSPAIMSASPGQKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPARFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85;
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   11605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11556 MW;
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                                                                                                                                                                                                                                                                                      G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G.M.,
                                                                                                                                                                                             HYBRIDOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYBRIDOMA
 WW.
                                                   FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2
FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3
FRAMEWORK 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                  OXAZOLONE
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
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COMPLEMENTARITY-DETERMINING
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 1CF3CE8D CRC32;
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                                       SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 444; LL
No. 6.1e-28;
17
                                                                                                                                                                                                                                                  (PHOX) ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PHOX) ANTIBODY
                                                                                                                                                                                                                                                                                        MILSTEIN C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MILSTEIN C.;
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KV6B_M
KV6B_M
AC P01676
AC P01676
AC P01676
DT 21-UUL
DT 01-OCT
DE IG KAP
OC EUTHER
RM [1]
RP SEQUEN
RA RAO D.
RA BICHE
CC PIF; A DOMAIN
FT DOMAIN
RESULT 7
KV6K_M
LOWER
LID KV6K_M
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Best Local S
Matches 84
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Best Local :
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DISULFID
NON_TER
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21-JUL-1986
01-OCT-1993
IG KAPPA CHA:
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DOMAIN
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BIOCHEMISTRY 17:5555-5559(1978).
-!- THIS CHAIN WAS ISOLATED FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE.
MEDLINE; 79082830
RAO D.N., RUDIKOFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KV6B_MOUSE
P01676;
                                                                                                                 IG KAPPA CHAÎN V-VI REGION
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDAT
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                             13-AUG-1987 (REL.
13-AUG-1987 (REL.
01-OCT-1993 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A01941; KVMSX4.
HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUS MUSCULUS (MOUSE)
EUKARYOTA; METAZOA;
  SEQUENCE FROM N.A. MEDLINE; 83271467. KAARTINEN M., GRIF
                                                                                                                                                                                                                                                                                                               P04945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                               KV6K_MOUSE
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JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)

KAPPA CHAIN V-VI REGION (XRPC 24).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGSGNSYSLTISSMEAEDAATYYCYQGSGYP-FTFGSGTKLEIK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGSGNSYSLTISSMEAEDAATYYCYQGSGYPFTFGSGTKLEIK 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTQSPAIMSASPGQKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLDSGVPARFSG
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     GRIFFITHS
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                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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23 33 48 55 87 96 106 106 107 107
                                                                                                                                                                               05, CREATED)
05, LAST SEQUENCE UPDATE)
27, LAST ANNOTATION UPDAT
VI REGION (NQ2-6.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHORDATA; VERTEBRATA;
                                                                                                                                            CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.9%;
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     G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPLEMENTARITY DETERMINING 1
FRAMEWORK 2.
COMPLEMENTARITY DETERMINING 2
FRAMEWORK 3.
COMPLEMENTARITY DETERMINING 3
FRAMEWORK 4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 412; DB 1;
Pred. No. 1.7e-25;
5; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 444; DB 1;
Pred. No. 6.1e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                            VERTEBRATA;
     MARKHAM
                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91B2CD6E CRC32;
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                                                                                                                                                                                                                                                                                                                                               108
     A.F.,
                                                                                                                                                                                                                                UPDATE)
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                                                                                                                                         TETRAPODA; MAMMALIA;
     MILSTEIN
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RESULT 8
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Best Local :
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Best Local
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DOMAIN 24 33 COMPLEME

DOMAIN 24 48 FRAMENOR

DOMAIN 34 48 FRAMENOR

DOMAIN 49 55 COMPLEME

DOMAIN 56 87 FRAMENOR

DOMAIN 88 98 COMPLEME

DOMAIN 99 108 FRAMENOR

DISULFID 23 87 BY SIMIL
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EMBL; K
HSSP; P
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DISULFID
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SEQUENCE
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                                                                                                                                                                                                                        RAO D.N., RUDIKOFF S., POTTER M.;
BIOCHEMISTRY 17:5555-5559(1978).
-!- THIS CHAIN WAS ISOLATED FROM
PIR; A01941; KVMSX4.
HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UF
01-CCT-1993 (REL. 27, LAST ANNOTATION
IG KAPPA CHAIN V-VI REGION (XRPC 44).
                                                                                                                                                                                                                                                                                                                                                                   KV6A_MOUSE P01675;
                                                                                                                                                                                                                                                              MEDLINE; 79082830 RAO D.N., RUDIKOFI
                                                                                                                                                                                                                                                                                                           MUS MUSCULUS (MOUSE)
EUKARYOTA; METAZOA; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                    EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                  MMUNOGLOBULIN V
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SGSGNSYSLTISSMEAEDAATYYCYQGSGYP-FTFGSGTKLEIK 105
                                             LTQSPAIMSASPGEKVTMTCSASSSVSNMHWYQQKSSTSPKLWYYDTSKLASGVPGRESG
                                                                                                                                                                                                                                                                                                                                                                                                                                   SGSGNSYSLTISSMEAEDAATYYCYQGSGYP--FTFGSGTKLEIK
                                  SGSATSYSLTITRMQAEDAATYYCQQWSSYPPMLTFGAGTKLELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTQSPAIMSASPGQKVTMTCSASSSVSYMYWYQQKPGSSPRLLIYDTSNLASGVPVRFSG
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K00746; G554059; -.
P01679; 1BAF.
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                                                                       Score 409; DB 1;
Pred. No. 2.9e-25;
7; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 410;
Pred. No. 2.
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 2.

COMPLEMENTARITY-DETERMINING
                                                                                                                                                COMPLEMENTARITY-DETERMINING FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
                                                                                                                                                                                     COMPLEMENTARITY-DETERMINING FRAMEWORK 2.
                                                                                                                                                                                                        FRAMEWORK 1
                                                                                                                                                                                                                                                                                                            VERTEBRATA; TETRAPODA;
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Best Local
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                                                                                                            MEDLINE: 81054757.

RUDIKOFF S., RAO D.N., G
PROC. NATL. ACAD. SCI. U
-!- THE TWO SEQUENCES AR
-!- THESE CHAINS WERE IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KV6C_MOUSE STANDARD; PRT; 107 AA P01677; P01677; 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDAT IG KAPPA CHAIN V-VI REGION (TEPC 601 AND TE MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
NON_TER
SEQUENCE
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DOMAIN
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DOMAIN
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RUDIKOFF S., RAO D.N., GLAUD PROC. NATL. ACAD. SCI. U.S.A-i- THIS CHAIN WAS ISOLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN V-VI REGION (SAPC 10).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MANNALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KV6D_MOI
P01678;
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                           PIR; A01941; KVMSX4.
HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A01941; KVMSX4.
HSSP; P01679; 2FBJ.
IMMUNOGLOBULIN V REG
                                                                                                                                                                                                                                    SEQUENCE (TEPC 191).
MEDLINE: 81054757.
                                                                                                                                                                                                                                                                                                                              BIOCHEMISTRY
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HSSP; P01679; 2FBJ.
MMWNOGLOBULIN V REGION
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                                                                                         GALACTAN.
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                                                                                                                                                                                                                                                                                                                        (TEPC 601).
79082830.
, RUDIKOFF S., POTTER M.
STRY 17:5555-5559(1978).
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79.8%;
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U.S.A. 77:4270-4274(1980).
LATED FROM A MYELOMA PROTEIN THAT BIND GALACTAN
                                                                                                                                                                          GLAUDEMANS C.P.J., POTTER U.S.A. 77:4270-4274(1980).
                                                                                                                                                    IDENTICAL
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COMPLEMENTARITY-DETERMINING 1
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2
FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3
FRAMEWORK 4.
BY SIMILARITY.
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                                                                                                                  FROM MYELOMA PROTEINS
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601 AND TEPC 191).
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.5e-25;
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RESULT 12
HV02_MOUSE STANDARD; PRT; 140 AA
ID HV02_MOUSE STANDARD; PRT; 140 AA
AC P01746;
DT 21-UUL-1986 (REL. 01, CREATED)
DT 21-UUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDAT
DE IG HEAVY CHAIN PRECURSOR V REGION (93G7).
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HV03_MOUSE
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Best Loc
Matches
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21-JUL-1986 (REL. 01, LAS
21-JUL-1986 (REL. 01, LAS
21-JUL-1986 (REL. 01, LAS
1G HEAVY CHAIN V REGION (
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAKOA; CHORD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                     NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE: 83131846.

SIEKEVITZ M., GETTER M.L., BRODEUR P., RIBLET R.,

MARSHAK-ROTHSTEIN A.;

EUR. J. IMMUNOL. 12:1023-1032(1982).

-I- FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED

THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL C

THESE V REGIONS HAVE REARRANGED TO THE SAME J SEGMENT, JH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HV03_MOUSE
P01747;
                                                                                                                                                                                                                                                                                     PIR; A02028; HVMSG7.
HSSP; P01789; 6FAB.
                                                                                                                                                                                                                                                                         IMMUNOGLOBULIN V REGION; ANTIARSONATE
                                                                                                                       180 PKFQGKASITADTSSNAAYLQLSSLTSEDTAVYYCASYYYYSAYYAMYYWGQGTSVTVSS
                                                                                                                                                                   120 VQLQQSGVELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIHPENGNTVYD
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Local Similarity
hes 82; Conserv
                                                                                                                                                                                                       Local Similarity
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                                                                                                             EKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVYYGGSYYFDYWGQGTTLTVSS
                                                                                                                                                     VQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYTKYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGSGNSYSLTISSMEAEDAATYYCYQGSGYP-FTFGSGTKLEIK
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                                                                                                                                                                                                16;
                                                                                                                                                                                                Score 406; DB
Pred. No. 5.7e
l6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8,
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Pred. No. 4.2e-
8; Mismatches
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING
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COMPLEMENTARITY-DETERMINING
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                                                                                                                                                                                                          DB 1;
.7e-25;
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Best Local Similarity
Matches 78; Conser
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SEQUENCE
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NON_TER
STRAND
                                                                                                                                                                                                                            21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN V-VI REGION (J539).
MUS MUSCULUS (MOUSE).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TET EUTHERIA; RODENTIA.
                                                                                                PROTEINS 1:74-80(1986)
-:- THIS CHAIN WAS ISO
PIR; A01942; KVMSJ5.
PDB; 2FBJ; 15-OCT-90.
                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDLINE; 88217852.
SUH S.W., BHAT T.N., NAVIA M.A., COHEN
DAVIES D.R.;
                                                                                                                                                                               MEDLINE: 81054757.
RUDIKOFF S., RAO D.N.,
PROC. NATL. ACAD. SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 82152818.
SIMS J., RABBITTS T.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A02028; HVMSG7.
HSSP; P01789; 6FAB.
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EMBL; J00493; G195007; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=A/J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUTHERIA; RODENTIA.
                                                                                        IMMUNOGLOBULIN
                                                                                                                                                                                                           SEQUENCE.
                                                                                                                                                                                                                                                                                           P01679;
                                                                                                                                                                                                                                                                                                   KV6E_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY; HYBRIDOMA;
                                                                                                                                                                                                                                                                                                                                                 132
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140 AA;
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 REGION;
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15514 MW;
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140
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                                                                                                                                                                                                                                     CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.6%;
                                                                                                                                                                              GLAUDEMANS C.P.J., POTTER M.;
U.S.A. 77:4270-4274(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESTESS
                                                                                       3D-STRUCTURE
                                                                                                                 FROM A MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 401.5; DB 1
Pred. No. 1.5e-24;
                                 COMPLEMENTARITY-DETERMINING FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING
                                                            COMPLEMENTARITY-DETERMINING FRAMEWORK 2.
                           FRAMEWORK
                                                                               FRAMEWORK 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G
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                                                                                                                                             COHEN
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                                                                                                                                             RUDIKOFF
                                                                                                                  BIND GALACTAN
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RESULT
HV07_MC
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Best Local
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HV07_MOUSE

FY01751; P01752;

21-JUL-1986 (REL. 01, CREATED)

21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

01-OCT 1996 (REL. 34, LAST ANNOTATION UPDATE)

01-OCT 1996 (REL. 34, REGION (B1-8 / 186-2).
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                                                                                                                                                                                                                                                                                                       BALTIMORE D.;
CELL 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                 IG HEAVY CHAIN PRECURSOR V REGION (B1-8 / 186-2).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA;
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                                                                                                                                                                                                                         PIR; A0
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        EMBL; J00529;
                                                                                                                                                                                                                                                                                                                                                                                                                    EUTHERIA; RODENTIA.
                                                                                                                                                                                             IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                        ·! - THE B1-8
                                                                                                                                                                                                                                                                                                                                     BOTHWELL A.L.M., PASKIND
                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 81234548
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                                                                                                                                                                                                                                                          ANTIBODIES!
                                                                                                                                                                                                                                                                        THE B1-8 MU CHAIN ANTIBODIES TO THE
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118
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11502 MW;
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401224412244
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                                                                                                                                                                                             SIGNAL.
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                               FRAMEWORK 3.
D SEGMENT.
JH2 SEGMENT.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                        AS CLONED FROM A HYBRIDOMA MAKING (4-HYDROXY-3-NITROPHENYL)ACETYL
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Pred. No. 1.2e-24;
                                                                                              FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING
                                                                                                                           COMPLEMENTARITY-DETERMINING
                                                                                                                                          IG HEAVY CHAIN V FRAMEWORK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF938E49 CRC32
DEB2C7DA CRC32
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                                                                                                                                                                                                                                                                                                                                     M., IMANISHI-KARI
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RESULT 15

KV4A_MA
AC P01680
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DT 21-GCT
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OC EUKARY.
OC EUTHER
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RA KWANN S
RL CELL 2
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CC KAN
DR EMBL;
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DR HSSP;
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FT CHAIN
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Jah time: 615 sec
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                                                                                          밁
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Best Local Similarity 78.1
Matches 82; Conservative
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Best Local Similarity
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EMBL; J00577; G196764; --
EMBL; V00780; E1181574; --
PIR; A01943; KVMS7B.
HSSP; P01679; 1FIG.
IMMUNOGLOBULIN V REGION; SIG
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NON_TER
SEQUENCE
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CHAIN
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21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
1G KAPPA CHAIN PRECURSOR V-IV REGION (S107B).
MUS MUSCULUS (MOUSE).
EUKARYOTA, METAZOA, CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 82115300.
KWAN S.-P., MAX E.E., SEIDMAN J.G., LEDER P.,
CELL 26:57-66(1981).
                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KV4A_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 DYWGQGTTLTVSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 YYWGQGTSVTVSS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26
                                                                                                                                                         THIS PROTEIN, IN WHICH THERE IS A DELETION OF TWO AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE NORMAL
                                                                                                                                                                                                                                                                                                                          129
129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                             129
45
57
72
711
111
118
128
                                                                                                                                                                                                                                                                                                                           13833 MW;
                                                                                                                                                                                                                                                31.18; 78.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.5%; Score 400; DB 1; Length 139; 58.6%; Pred. No. 1.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                 Score 395; DB 1; Length 129; Pred. No. 4.3e-24; 7; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG KAPPA CHAIN V-IV REGION (S107B).
FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                           COMPLEMENTARITY-DETERMINING 3. FRAMEWORK 4.
                                                                                                                                                                                                                                                                                                                                                                                                              COMPLEMENTARITY-DETERMINING 2. FRAMEWORK 3.
                                                                                                                                                                                                                                                                                                                        8D4D8311 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                           SIMILARITY.
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Title:
Perfect score:
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    SPTREMBL_8:*
1: sp_inugal:
2: sp_inuvert
4: sp_invert
4: sp_manmal:
5: sp_organe
6: sp_organe
7: sp_phage:
8: sp_plant:
9: sp_bacter
10: sp_roden
11: sp_virus
12: sp_uncla
14: sp_uncla
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1271
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: sp_mhc:*
: sp_organelle:*
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: sp_virus:*
: sp_vertebrate:*
: sp_unclassified:*
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Copyright (c) 1993 - 1998 Compugen Ltd.
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sp_invertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4. £	43	42	40	39	38	37	36	35	34	33	32	31	30
125.5	127	129.5	130	130.5	131.5	131.5	131.5	132	133	133.5	134	134	135
9.9	10.0	10.2	10.2	10.3	10.3	10.3	10.3	10.4	10.5	10.5	10.5	10.5	10.6
509	133	254	418	145	258	503	50	78	158	398	250	258	509
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035924	Q31178	090557	070426	Q16237	Q90559	P78324	Q15533	075720	Q90531	000241	Q90569	Q90556	P97710
035924 mus musculu	Q31178 mus musculu	Q90557 ginglymosto	070426 rattus norv	Q16237 homo sapien	Q90559 ginglymosto	P78324 homo sapien	Q15533 homo sapien	075720 homo sapien	Q90531 ginglymosto	000241 homo sapien	Q90569 ginglymosto	Q90556 ginglymosto	P97710 rattus norv

ALIGNMENTS

RES DT DT DT RES DT	Qy Db	PRES PRES PRES PRES PRES PRES PRES PRES
RESULT 2 Q15535 Q15535 PRELIMINARY; PRT; 100 AA. AC Q15535; DT 01-NOV-1996 (TREMBLREL. 01, CREATED) DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) DT V KAPPA (FRAGMENT). OS HOMO SAPIENS (HUMAN). OC CHTARRYINI; HOMINIDAE; HOMO. RN [1] RP SEQUENCE FROM N.A. RA KATO S., TACHIBANA K., TAKAYAMA N., KATAOKA H., YOSHIDA M.C., RA TAKANO T.; RL SUBMITTED (SEP-1990) TO EMBL/GENBANK/DDBJ DATA BANKS.	Query Match Best Local Similarity 79.0%; Pred. No. 9.6e-26; Matches 83; Conservative 8; Mismatches 12; Indels 2; Gaps / SITOSPAINSASPGEKVTMTCSASSSVSNMHWYQOKSSTSPKLMVYDTSKLASGVPGRE 60	RESULT 1 PRO913; PRELIMINARY; PRT; 130 AA. PRO913; DT 01-NOV-1998 (TREMBLREL. 08, CREATED) DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE) DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) DC IG KAPPA CHAIN V REGION PRECURSOR. SUUS MUSCULUS (MOUSE). CE UKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; CE CULARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; CE CULARYOTA; MURIDAE; MURINAE; MUS. RI (1) RI (1) RI (1) RI (2) RI (3) RI

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ID C75724

AC C77

DT C77

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Best Local :
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Best Local
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01-NOV-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
1G HEAVY CHAIN VARIABLE R
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01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
IG HEAVY CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Human IgA and IgM secreting intestinal plasma cells mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                            HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                           075741
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
FISCHER M.,
                      TISSUE-INTESTINE;
                                             SEQUENCE FROM N.A.
                                                                                          PRIMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 YIHWVKQRPEQGLEWIGWIHPENGNTVYDPKFQGKASITADTSSNAAYLQLSSLTSEDTA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                         211 VYYCA----SYYYYSAYYAMYYW 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YWTWIRQPPGKGLEWIGFIY-YSGNTNYNPSLKSRLTISVDTSKNQFSLKLTSMTAADTA 61
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37; Conserv
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                                                                                        CATARRHINI;
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100 AA;
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                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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10871 MW;
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42.3%;
                                                                                        HOMINIDAE;
                                                                                                                                                                     08, CREATED)
08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDAT
REGION (FRAGMENT).
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08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDAT
REGION (FRAGMENT).
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Pred. No. 6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 212; DB 2;
Pred. No. 1.1e-09;
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                                                                                                              VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                   85
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                                                                                                            EUTHERIA;
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075734;
1 01-NOV-1998 (TREMBLREL. 08,
7 01-NOV-1998 (TREMBLREL. 08
01-NOV-1998 (TREMBLREL. 08
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Best Local :
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Best Local
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075736;
01-NOV-1998
01-NOV-1998
01-NOV-1998
PRIMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FISCHER M., KUEPPERS R.;
"Human IgA and IgM secreting intestinal plasma cells
mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ009534; E1311466; -.
NON_TER 1 1
NON_TER 81 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Human IgA and IgM secreting intestinal plasma cells carry heavily mutated VH region genes.";
SUBMLITIED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ009540; E1311476; ...
NON_TER 1 1
NON_TER 77 77
SEQUENCE 77 AA; 8734 MW; 1F7F9E8E CRC32;
                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE |
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATIO)
IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                             210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 IHWVKQRPEQGLEWIGWIHPENGN--TVYDPKFQGKASITADTSSNAAYLQLSSLTSEDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 CASYYYYSAYYAMYYW 229
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                                                                                                                                                                                                                                                                                                                                                                          AVYYCASY--YYYSAYYAMYYW
                                                                                                                                                                                                                                                                                                                                                  AVYYCVAYEGYY - - - YYGMDAW
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35; Conserv
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37; Conservative
                     CATARRHINI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 AA;
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9375 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.3%;
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                       HOMINIDAE;
                                                                                                             08, CREATED)
08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 181.5; DB 2;
Pred. No. 1.8e-07;
3; Mismatches 25;
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Pred.
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                                                                                                                                                                                                                                PRT;
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No. 1
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L.5e-07;
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RESULT
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      Query Match
Best Local Similarity
Matches 30; Conserv
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
IG HEAVY CHAIN VARIABLE
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TISSUE=INTESTINE;
FISCHER M., KUEPPE
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mutated VH region genes.";
SUBMITIED (JUL-1998) TO EMBL/GENBANK/DDBJ
EMBL; AJ009523; E1311446; ".
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          219
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9040
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42.5%;
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08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDAT
REGION (FRAGMENT).
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                                                            08, CREATED)
08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDAT
REGION (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
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Pred. No. 4.4e-07;
7; Mismatches 23
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SEQUENCE FROM N.A.
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NON_TER 82 82
SEQUENCE 82 AA; 9566 MY
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SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
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Pred. No. 4.7e-07;
4; Mismatches 22;
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8; Mismatches
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Pred. No. 6
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SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ
EMBL; AJ009524; E1311448; -.
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mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ
EMBL; AJ009525; E1311450; -.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
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. 08, LAST ANNOTATION
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LAST SEQUENCE UI

LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 174; DB 2;
Pred. No. 6.3e-07;
5; Mismatches 22
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Pred. No. 6.6e-07;
5; Mismatches 24
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                                   PRT;
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Matches 31
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Best Local
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O75733;
O1-NOV-1998 (TREMBLREL 0
O1-NOV-1998 (TREMBLREL 0
O1-NOV-1998 (TREMBLREL 0
IG HEAVY CHAIN VARIABLE R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Human IgA and IgM secreting intestinal plasma cells mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ009537: E1311470; -.

NON_TER 1 1 1
NON_TER 72 72
SEQUENCE 72 AA; 8345 MJ. ----
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01-NOV-1998
01-NOV-1998
IG HEAVY CHA.
                                                                                                                             NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                "Human IgA and IgM secreting intestinal plasma mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA
                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VEI
PRIMATES; CATARRHINI; HOMINIDAE;
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                           EMBL; AJ009530; E1311460;
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                                                                                                                                                                                                  ISCHER M., KUEPPERS
                                                                                                                                                                                                                                                                                                                                                                                                                     152 IHWVKQRPEQGLEWIGWIHPENGN--TVYDPKFQGKASITADTSSNAAYLQLSSLTSEDT
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 AVYYCA--
                                       IHWVRQTSGKGLEWVARIRSKTHSYATAYAASVEGRFVVSRDDSKNTAYLQMNSLKSEDT
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31; Conservative
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1998 (TREMBLREL. (
1998 (TREMBLREL)
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METAZOA; CHORDATA; VERTEBRATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                               76
                                                                              Conservative
                                                                                                                               76
6 AA;
-AGSSSEYW
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                                                                                     13.2%;
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E REGION (FRAGMENT).
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08, LAST ANNOTATION UPDATE)
REGION (FRAGMENT).
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 76
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                            Score 168; DB
Pred. No. 1.8e
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 171; DB
Pred. No. 9.9e
L6; Mismatches
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.8e-06;
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RESULT

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O75740
ID O75740;
DT O1-NOV-DT O1-NOV-DT O1-NOV-DE IG HEAV
OS HOMO SA
OC EUKARYO
OC PERMATE
RN [1]
RP SEQUENC
RC TISSUE-RA [1]
RP FISCHER
RT "Human
RT mutated
RL SUBMITT
DR NON_TER
SQ SEQUENC
SQ SEQUENC
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         80
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Best Local Similarity
Matches 31; Conserv
                                                                                                  Query Match 13.1%;
Best Local Similarity 40.5%;
Matches 32; Conservative 2
                                                                                                                                                                          NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FISCHER M., KUEPPERS R.;
"Human 19A and 19M secreting intestinal plasma cells carry heavily mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ009539; E1311474; -.
NON_TER 1 1
NON_TER 86 86
SEQUENCE 86 AA; 9625 MW; 07627E8C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
VH.
                                                                                                                                                                                                                    TISSUE-INTESTINE;
FISCHER M., KUEPPERS R.;
"Human IgA and IgM secreting intestinal plasma cells carry heavily mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ009538; E1311472; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                         HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 TAVYYCAS 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 YIHWVKQRPEQGLEWIGWI--HPENGNTVYDPKFQGKASITADTSSNAAYLQLSSLISED 208
211 VYYCASYYYYSAYYAMYYW 229
                                                        151 YIHWVKQRPEQGLEWIGWIHPENGNTVYDPKFQGKASITADTSSNAAYLQLSSLTSEDTA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 TAVYYCTT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 WMNWVRQAPGKGLEWVGRIKSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTED 62
                                       1 YMSWIRQSPGKGLEWIGYIY-YTGSINYNPSLKSRVTISLGTSENQFSLNLTSVTAADTA 59
                                                                                                                                                                           78 AA;
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                                                                                                   20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 167; DB 2; I
Pred. No. 2.4e-06;
.5; Mismatches 20;
                                                                                                  Score 166; DB 2; 1
Pred. No. 2.6e-06;
10; Mismatches 23;
                                                                                                                                                                           05D273B9 CRC32;
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Search completed: May 13, 1999, 10:05:19 Job time: 657 sec

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Anti-human SC sing Fv(GP-4) immunosup

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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OM protein protein search, using sw model

Run on: May 13, 1999, 10:02:41; Search time 23.53 Seconds (without alignments) 206.293 Million cell updates/sec

Title: Perfect score:

Sequence: US-08-704-178-4 1271 1 MQLTQSPAIMSASPGEKVTM.....SAYYAMYYWGQGTSVTVSSY 240

Scoring table: BLOSUM62

Searched: 162890 seqs, 20225328 residues

Database : A_Geneseq_34:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	321	Result No.
821.5 795.5 795.5 795.5 763 7752 752 752.5 7725.5 7725.5 7725.5 7725.5 7725.5 7725.7 7727 7727 772	126 125 125	
55.0.00 1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.	יבים	% Query Match
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RR12798 RR151842 R15482 R45482 R45482 R45483 R45784 W111508 W115084 W125783 W125783 W125783 W1256649 R056646 W1256650 W1266650 W1266650 W126667 W126667 W126671 R43677 R43677 R736649 W126680 R736649	518 544 078	ID
NWB3 light inti-erable equence of ingle chai lingle ch	~ ၉ ဌ ¦	Descript
assingstance of Lorungononov, substance at t	ain anti- of the si	

PSC Claim 2; Columns 27-30; 28pp; English. CC The present sequence represents a claimed single-chain antibody, cd designated e21[Fv], which binds to erbB-2. Monoclonal antibody e21 CC was generated by immunising mice with N/erbB-2 cells overexpressing CC the gp185 protein, removing spleen cells and producing hybridomas CC monoclonal antibody was isolated and converted to cDNA. Regions CC coding for the heavy- and light-chain variable regions were then CC amplified by PCR and joined via a sequence encoding a peptide CC linker. The resulting single-chain antibody is useful for in vitro CC diagnosis of tumour cells which overexpress the erbB-2 gp185 CC marker, e.g. breast, overian and non-small cell lung carcinomas, CC and, when coupled to a cytotoxic agent, to treat such tumours.	SULT 1 \$186 standard; W15186; W15186; 05-JUN-1997 (fi Single-chain ant Single-chain ant Single chain ant Dreast cancer; o immunodiagnosis; Mus musculus. Synthetic.

Qy 밁 ρ 밁 ğ В B δÃ Query Match 99.4%; Score 1264; DB 1; Length 239; Best Local Similarity 100.0%; Pred. No. 4.5e-82; Matches 239; Conservative 0; Mismatches 0; Indels 181 KFQGKASITADTSSNAAYLQLSSLTSEDTAVYYCASYYYYSAYYAMYYMGQGTSVTVSS 239 121 QLQQSGVELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIHDENGNTVYDD 180 181 KFQGKASITADTSSNAAYLQLSSLTSEDTAVYYCASYYYYSAYYAMYYWGQGTSVTVSS 239 121 QLQQSGVELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIHPENGNTVYDP 180 0; Gaps 0;

RESULT R45443

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Best Local Similarity
Matches 238; Conserv
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21-OCT-1992;
30-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Fig 8; 37pp; English.

The source of human erbB-2 protein for the prodn. of antibodies no 23 and 21 (Q55180/R45442; Q55181/R45443) is a NIH/3T3 cell engineered to express the human erbB-2 protein on its surface (N/erbB-2). Abs no. 21 and 23 are directed against the extracellular domain of gp185 erbB-2. Nude mice manipulated to produce rapidly growing tumours were used in a trial of the efficacy of the Abs. I animals given a combination of the 2 Abs, tumours completely regressed after 11 days.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1994 (first entry)
Sequence of the single cha
Single chain anti-erbB1 an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R45443
R45443;
                                                                                                                                   26-OCT-1994.
21-APR-1994; 106257.
21-APR-1993; JP-094491.
07-MAR-1994; JP-036065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treatment of malignancies over 2 monoclonal antibodies which
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(MOLE-) MOLECULAR ONCOLOGY
Kasprzyk PG, King CR;
WPI; 94-025878/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
WO9400136-A.
                                                             Takeshita
WPI; 94-32
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 Immunosuppressant
interleukin-2 resp
                                         N-PSDB; Q73678.
                                                                                                  Hamura
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                                                                                                                                                                                                                                                                                                           Fv (GP-2)
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R60780;
                                                                                                                  (AJIN )
                                                                                                                                                                                                                                                  mmunosuppressive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
                                                                                                                                                                                                                                                                   GP-2) immunosuppressive.
; monoclonal antibody; hybridoma;
antibody variable region; GP-2; i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLTQSPAIMSASPGEKVTMTCSASSSVSNMHWYQQKSSTSPKLWVYDTSKLASGVPGRFS
                                                           94-325948/41.
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                                                                                                                  AJINOMOTO
                                                                                                Kanayama
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                                                                                        TY,
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l antibody; cancer therapy; preventio
                                                                                                  Nakazawa
                                                                                                                                                                                                                                                                                                                                                                  244
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nich recognise different
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Pred. No. 1e-81;
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                     ability
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                                                                                                Shimamura
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PROBLEM PROBLE
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Best Loc
Matches
                                                                                                                                       28-MAY-1991.
11-JAN-1990;
11-JAN-1990;
(USSH) NAT I
                            Rapid
by fus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
region
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OVB3 light and heavy chains.
Immunoglobulin; immunotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R12798
R12798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page 26-27; 37pp; English.

MAB capable of binding to the gamma chain of the IL-2 recept
thus of blocking the IL-2 response, is produced by mouse byt
line GP-2 (FERM BP-4641). DNA encoding the variable region
this MAB was expressed in E. coli, yielding Fv(GP-2) with
immunosuppressive activity.
Sequence 244 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pseudomonas
Synthetic.
                                                                                                                                                                                                                                   US7463111-A.
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       fusing genes with rget cells
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in 1;
91-200877/27.
93-200877/27.
DB; Q12405.
d cloning of antibody genes as single chain immuno-toxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTQSPAIMSASPGEKYTMTCSASSSVSN--MHWYQQKSSTSPKLWVYDTSKLASGVPGRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTQSPSIMSASLGERVTMTCTASSSVSSSYLHWYQQKPGSSPKLWIYSTSNLASGVPARF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VKLEESGSELVRPGASVKLSCKASGYTFTSYWMHWVKQRHGQGLEWIGNIYPGSGSTNYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunotoxin; antibody;
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                                                                                                                                                                                                                                                                                                                                            219. .229
/label- CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         170. .186
/label - CDR2
                                                                                                                                                                                                                                                                             /label= N-terminal
121. .134
                                                                                                                                                                                                                                                        /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label Light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            labe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label- Heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                        label=
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                                                                                                                                            HEALTH
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68.3%;
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l- CDR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 829.5; DB 1;
Pred. No. 1.4e-51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            variable region;
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RESULP RE
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                                                                                                                                                                                     inhibition of proliferation or survival of, esp. malignant erbB2, realls - by introducing nucleic acid mol. encoding antibody homologue which is expressed and binds, pref. erbB2, protein intracellularly bisclosure; page 29-30; 48pp; English.

A nucleic acid comprises a first sequence encoding a signal peptide (R94019) linked to a second sequence (T17728) encoding a single chain Fv fragment (R94020) that binds a human erbB2 oncoprotein.

The anti-erbB2 sFv portion is obtained by PCR using e23scFv plasmid as template. The signal peptide directs the scFv to the endoplasmic reticulum. The nucleic acid is incorporated into a plasmid or viral vector to facilitate expression of the scFv antibody homologue within e.g. an epithelial carcinoma cell. Intracellular expression of the homologue inhibits surface expression of erbB2 and thereby inhibits cell proliferation and cell survival and decreases
  Query Match
Best Local S
Matches 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Best L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAR-1996.
23-AUG-1995; U10740.
06-SEP-1994; US-30139.
06-JUN-1995; US-468252.
(UABR-) UAB RES FOUND.
CUTIEL DT, DESHANE J;
WPI; 96-171307/17.
N-PSDB; T17728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence comprises the L and H chains of murine MAb OVB3, joined together via a linker. The sequence is encoded by clone povB3158-1 in which the 3' end of the DNA is linked to the 5' end of the coding sequence for PE40, a Pseudomonas exotoxin lacking domain I. The protein expressed by the clone can be used to kill specific target cells.

Sequence 241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy.
Synthetic.
                                                                                                                                                tumorigenicity.
Sequence 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oncoprotein; erbB2; cell proliferation; tumour; cancer; intracellular antibody homologue; single chain antibody; scFv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R94020 standard; Protein;
                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQQSGVELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIHPENGNTVYDPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGSGNSYSLTISSMEAEDAATYYCYQGSGYPFTFGSGTKLEIK-GSTSGSGKSSEGKGVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -FQGKASITADTSSNAAYLQLSSLTSEDTAVYYCASYYYYSAYYAMYYWGQGTSVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVESGGGLVQPGGSRQLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYI-SRGGNTIYYAN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGSGNSYSLTISSMEAEDVATYYCFQGSGYPYTFGGGTKLELKEGKSSGSGSESKVDDVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTQSPAIMSASPGEKVTMTCSAISTVSYMHWYQQKSSTSPKLWIYETSKLASGVPGRFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVKGRFTISRDNPKNTLFLQMTSLRSDDTAMYYCARSHYYGYFYAMDYWGQGTTLTGSS
     155;
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                               62.6%;
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     32;
                               Score 795.5; DB Pred. No. 3.3e-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 821.5; DB 1
Pred. No. 5.1e-51;
1; Mismatches 47
     Mismatches
5; DB 1;
3.3e-49;
hes 45;
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  9;
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MQLTQSPAIMSASPGEKVTMTCSASSSVSNMHWYQQKSSTSPKLWVYDTSKLASGVPGRF

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61

SGSGSGNSYSLTISSMEAEDAATYYCYQGSGYPFTFGSGTKLEIKGSTSGSGKSSEGKGV

LQLTQSPAILSASPGEKVTMTCRATPSVSYMHWYQQKPGSSPKPWIYTTSNLASGVPARF

60

62

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PT cells expressing this protein
PS Claim 2; Columns 25-28; 28pp; English.

CC The present sequence represents a claimed single-chain antibody,
CC designated e23(FV), which binds to erbB-2. Monoclonal antibody e23
CC was generated by immunising mice with N/erbB-2 cells overexpressing
CC the gp185 protein, removing spleen cells and producing hybridomas
CC by standard techniques. Messenger RNA coding for the anti-erbB-2
CC monoclonal antibody was isolated and converted to CDNA. Regions
CC coding for the heavy- and light- chain variable regions were then
CC amplified by PCR and joined via a sequence encoding a peptide
CC linker. The resulting single-chain antibody is useful for in vitro
CC diagnosis of tumour cells which overexpress the erbB-2 gp185
CC marker, e.g. breast, ovarian and non-small cell lung carcinomas,

cc and when coupled to a cytotoxic agent, to treat such tumours.
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                                                           Query Match
Best Local :
                                             Matches
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07-OCT-1991; 772270.
07-OCT-1991; US-772270.
07-OCT-1991; US-906555.
30-JUN-1992; US-906555.
14-MAY-1993; US-061092.
                                                                                                                                                                                                                                                                                                                                                        Single chain antibodies specific for erbB-2 protein, gp185 labels or cytotoxin, useful for detection and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                       Bird RE, Kasprzyk PG, King WPI; 97-064831/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single chain antibody; variable region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single-chain
                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; T65006.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W15185
                                                                                                                                                                                                                                                                                                                                                                                                                                      (ARON-) ARONEX PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunodiagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KFQGKASITADTSSNAAYLQLSSLTSEDTAVYYCA---SYYYYSAYYAMYYWGQGTSVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGLINPYNGDTNYNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLQQSGVELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIHPENGNTVYDP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIKGSTSGSGKSSEGKGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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                                                           Similarity
                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-erbB2 antibody e23(FV).
antibody; variable region; light chain; heavy chain;
antibody; variable region; light chain; heavy chain;
r; ovarian cancer; non-small cell lung carcinoma;
sis; treatment; cytotoxic agent; erbB-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 108. .121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein; 237
                                                          62.6%;
                                           32;
                                                        Score
Pred.
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                                           Mismatches
                                                        795.5;
No. 3.3
                                                          5; DB 1;
3.3e-49;
                                          Indels
                                                                        Length
                                          9;
                                          Gaps
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                                                                                                                                                                                    Query Match
Best Local S
Matches 154
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21-OCT-1992; U08545.
30-JUN-1992; US-906555.
(MOLE-) MOLECULAR ONCOLOGY II
Kasprzyk PG, King CR;
WPI; 94-025878/03.
                                                                                                                                                                                                                              The source of human erbB-2 protein for the prodn. of antibodies : 23 and 21 (Q55180/R45442; Q55181/R45443) is a NIH/3T3 cell engineered to express the human erbB-2 protein on its surface (N/erbB-2). Abs no. 21 and 23 are directed against the extracellular domain of gp185 erbB-2. Nude mice manipulated to produce rapidly growing tumours were used in a trial of the efficacy of the Abs. animals given a combination of the 2 Abs, tumours completely regressed after 11 days.
                                                                                                                                                                                                                                                                                                                           gp185
                                                                                                                                                                                                                                                                                                                                                                                                                     monoclonal antibody.
Synthetic.
WO9400136-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1994 (first entry)
Sequence of the single chain anti-
Single chain anti-erbBl antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R45442;
21-JUL-1994
                                                                                                                                                                                                                                                                                                                                      2 monoclonal
                                                                                                                                                                                                                                                                                                                                              Treatment of malignancies
                                                                                                                                                                                                                                                                                                                                                       N-PSDB; Q55180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R45442 standard;
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                                                                                   QLQQSGVELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIHPENGNTVYDP
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                                            KFQGKASITADTSSNAAYLQLSSLTSEDTAVYYCA---SYYYYSAYYAMYYWGQGTSVTV
                                                                                                                      SGSGSGNSYSLTISSMEAEDAATYYCYQGSGYPFTFGSGTKLEIKGSTSGSGKSSEGKGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGLINPYNGDTNYNQ
                                    KFKGKATFTVDKSSSTAYMELLSI
                                                                       QLQDSGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGLINPYNGDTNYNQ
                                                                                                            SGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIKGSTSGSGKSSEGKGV
                                                                                                                                                 LQLTQSPAILSASPGEKVTMTCRATPSVSYMHWYQQKPGSSPKPWIYTTSNLASGVPARF
                                                                                                                                                                                     154;
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                 238
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                                                                                                                                                                                              Similarity
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                      antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                             62.2%;
                                                                                                                                                                                                                                                                                                                                      which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236
                                                                                                                                                                                                                                                                                                                                    over-expressing ERB-[2 - using at hich recognise different epitopes of
                                                                                                                                                                                    32;
                                                                                                                                                                                    Score 790.5;
Pred. No. 7.5e
32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-erbB2 antibody,
body; cancer therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₽
                                                                                                                                                                                              .5e-49;
                                                                                                                                                                                                      BB
                                                                                                                                                                                    46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ab no.23. prevention;
                                                                                                                                                                                                    Length
                                                                                                                                                                                    Indels
                                    WGAGTTVTV
                                                                                                                                                                                                      236;
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                                                                                                                                                                                                                                                                                                         no
                                                                                                                                                                                    Gaps
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WERSULT WARRESTER ACT OF STATE OF STATE
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Lie rv fragment encoded by pSCVI was able to proceed infection by HRV-14. It was less active than mod conditions and a Gly-Gly-Gly-Gly-Gly-Ser flexible lift and H chains as either a monomer or a dimer see also R15437-R15442.

Sequence 240 AA.
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Best Local S
Matches 149
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Homo sapiens.
EP-459577-A.
04-DEC-1991.
25-MAY-1991; 201243.
01-JUN-1990; US-532001.
(MERI ) MERCK & CO INC.
Colonno RJ, Condra JH, T
WPI; 91-355850/49.
                                                                                                                                                                                                                                                                                                                              22-DEC-1997 (first entry)
Anti-gpl30 antibody derived scFv.
Anti-gpl30 antibody; e. coli; anti-T3
single chain Fv; scFv; antibody; E. coli; anti-T3
anti-gpl30 antibody; inclusion body; chaperonin.
Synthetic.
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R15443;
25-FEB-1992
Single chain
Producing single chain Fv antibody in Escherichia coli - by expression in an inclusion body, followed by protein folding co-expression with a chaperonin as a soluble fraction Claim 4; Page 6-7; 9pp; Japanese.

The sequences given in W25783-84 represent single chain Fv (santibodies which are produced in E.coli. The scFV's are deri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microbially expressed portions attachment of rhinovirus ligand molecule (ICAM-1)
                                                                                                                                                         (TOYJ ) TOSOH CORP. WPI; 97-474306/44. N-PSDB; T91615.
                                                                                                                                                                                                                                  15-FEB-1996; 027622.
15-FEB-1996; JP-027622.
                                                                                                                                                                                                                                                                                        26-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-SEP-1997 (first entry)
Single chain anti-Fc gamma RI antibody fused to anti-CEA
Humanised antibody; anti-Fc receptor; H22; bifunctional;
fusion protein; chimera; carcinoembryonic antigen; CEA.
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          07-JUN-1996; 661052.
07-JUN-1996; US-661052.
07-JUN-1995; US-6484172.
(MEDA-) MEDAREX INC.
Deo YM, Goldstein J, Graziano R, Soma WPI; 99-023374/02.
N-PSDB; V08176.
Specific killing of tumour cells - us Specific killing of tumour cells - us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1996; U09988
07-JUN-1995; US-484172.
(MEDA-) MEDAREX INC.
Deo YM, Goldstein J, G
                                                                                                                                                      Jb-JAN-1999 (first entry)
H22-anti-CEA antibody construct 321.
Multispecific single chain antibody; antibody H2
antibody-dependent cellular cytotoxicity; ADCC; epidermal growth factor receptor; breast cancer; Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-DEC-1996;
07-JUN-1996;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           also comprise an anti-target portion, used for the treatment of cancer, autoimmune disease and pathogenic infection Example 8; Fig 40; 115pp; English.

A mammalian expression construct encoding a single chain antibody having binding specificity for Fc gamma RI, derived from the humanised anti-Fc gamma RI monoclonal antibody H22 was prepared (see T58129). A bispecific single chain polypeptide was produced by fusing the H22 ScFv to an anti-carcinoembryonic antigen (CEA) antibody. The H22-anti-CEA fusion protein was shown to bind both Fc gamma RI and CEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fc gamma
Sequence
                                                                                                                                                                                                                              W73223;
25-JAN-1999
specific killing of tumour cells - using comprising an anti-Fc receptor antibody a
                                                                                                                                                                                                                                                              W73223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant, multi-specific anti-Fc receptor antibody molecules also comprise an anti-target portion, used for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 97-052242/
N-PSDB; T58130.
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                                                                                                                                              JS5837243-A.
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                                                                                                                                                                                                                                                                                                                               YYMGQGTSVTVSS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKSSEGKGVQLQQSGVELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIHP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGVPGRFSGSGSGNSYSLTISSMEAEDAATTYCYQGSGY--PETFGSGTKLEIKGSTSGS 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGSD----IKLQQSGAELVRSGTSVKLSCTASGFNIKDSYMHWLRQGPEQGLEWIGWIDP
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                                                                                                                                                                                                                                                                                                                                                                                                                     ENGNTVYDPKFQGKASITADTSSNAAYLQLSSLTSEDTAVYYC----ASYYYYSAYYAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCHQ---YLSSWTFGQGTKVEIKSSCSSG
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"6 histidine residues"
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Pred. No. 9.4e-46;
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                                                        Somasundaram
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                                                                                                                                                                                   antibody H22; tumour cell; therapy;
city; ADCC; HER 2/neu; infection;
and a portion which binds
             a multi-specific molecule
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RESULT
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PS Example 8; Fig 40; 57pp; English.

CC This sequence represents the construct 321, which is a fusion between an CC anti-CEA antibody and a multispecific single chain antibody designated CC 422. The antibody can be used in the method of the invention for inducing CC antibody-dependent cellular cytotoxicity (ADCC) against a tumour cell CC which is characterised by overexpression of HER 2/neu or epidermal growth CC factor receptor (EGFR), comprises contacting the tumour cell with a CC multispecific protein molecule (preferably a single chain antibody) CC comprising: (a) an anti-FC receptor antibody or an antigen binding CC fragment; (b) a portion which binds to HER 2/neu; and (c) a portion which binds to EGFR. The method can be used for treating cancers especially CC breast cancer or ovarian cancer. The multispecific antibody can also CC be administered prophylactically to vaccinate a subject against infection CC by a target cell.
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Best Local Similarity
Matches 154; Conserv
                                                                                                                                           21-MAY-1996.
02-SEP-1986; US-902971.
02-SEP-1986; US-902971.
02-SEP-1987; US-902110.
19-JAN-1989; US-299617.
25-APR-1999; US-512910.
01-APR-1993; US-40404.0
06-JUN-1995; US-468988.
(ENZO-) ENZON LABS INC.
Immunoassay using single chain antigen binding for labelled or immobilised antibody, are less to engineer, more stable and less expensive Example 9; Fig 39A-B; 78pp; English.

Computer-designed construct 18-2-3/TRY202' (W02 the DNA sequence given in T36463, comprises the
                                                                                                           (ENZO-) ENZON LABS INC.
Bird RE, Hardman K, Ladner RC;
WPI; 96-259060/26.
                                                                                                                                                                                                                                                                                                                                             single chain antibody; immunoassay;
single chain binding protein.
                                                                                                 N-PSDB; T36463
                                                                                                                                                                                                                                                                                                US5518889-A.
                                                                                                                                                                                                                                                                                                            Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                Chimeric Mus musculus;
                                                                                                                                                                                                                                                                                                                                                                             Antibody engineering; monoclonal antibody; MAb;
                                                                                                                                                                                                                                                                                                                                                                                                                            W02191 standard; Protein; 239 W02191;
                                                                                                                                                                                                                                                                                                                                                                                          13-NOV-1996 (first entry)
18-2-3/TRY202' single chain binding protein.
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Pred. No. 9
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.4e-46;
 (W02191), encoded by the variable regions
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                                                                              mol.
                                                                   immunogenic,
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RESULT
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                                                                                 DR N-PSDB; Q5150.

PPT Single chain polypeptide for binding antigen - comprising light PPT and heavy chain antigen binding portions linked by peptide linker PS Example 9; Figure 39; 78pp; English.

CC The single chain polypeptide is derived from the mature light and CC chain variable region of a monoclonal antibody (MAD) and has affinity CC for a given antigen (Fluorescein). It comprises a first CC chain variable region of an antibody and a second polypeptide comprising the antigen binding portion of of the light CC comprising the antigen binding portion of the heavy chain variable region of an antibody and a second polypeptide comprising the antigen binding portion of the heavy chain variable cregion of an antibody and at least one peptide linker linking the CC first and second polypeptide chains. The resulting single chain CC polypeptide can be used in diagnostics, therapy CC (in vivo and in vitro), imaging, purifications and biosensors. This particular single chain binding molecule was designated CC 18-2-3/TR202' and contains one linker peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
Query Match
Best Local Similarity
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02-SEP-1986; US-902971.
02-SEP-1986; US-902971.
02-SEP-1987; US-092110.
19-JAN-1989; US-299617.
25-APR-1990; US-512910.
(ENZO-) ENZON INC.
Bird RE, Hardman K; La
WPJ; 93-367875/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the light and heavy chains of anti-fluorescein monoclonal antibody (Mab) 18-2-3 linked by a peptide designed to fit into a groove on the backside of the variable domain structure. The DNA construct was inserted into vector pGX3703 and introduced into E. coli. 18-2-3/TRY202' was produced as a single chain molecule. It exhibited biological binding activity equivalent in specifically and affinity to that of the original Mab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R43679 standard;
R43679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single chain polypeptide with affinity for fluorescein. Monoclonal antibody; MAD; affinity; binding; antigen; diagnostics; therapy; imaging; purification; biosensors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KFQGKASITADTSSNAAYLQLSSLTSEDTAVYYCASYYYYSAYYAMYYWGQGTSVTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGSGSGNSYSLTISSMEAEDAATYYCYQGSGYPFTFGSGTKLEIKGSTSGSGKSSEGKGV 120
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148; Conser
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 58.98;
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Score 748.5; DB 1
Pred. No. 6.7e-46;
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Pred. No. 4.1e-46;
0; Mismatches 55;
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                                  밁
                                                                                                                                                                                                                                                                      Immuno:purifien. using single binding chain molecule including antigen-binding parts of antibody light and heavy chain variable regions connected by a linker - is smaller, stabler and less expensive than complete antibodies

Example 9; Fig 39; 78pp; English.

A DNA construct (T13739) codes for single chain binding molecule 18-2-3/TRY202' (R99649), in which VL and VH regions of anti-11 conscein monoclonal antibody 18-2-3 are joined by a peptide 11 linker composed primarily of alternating Gly and Ser residues, with 11 clinker composed primarily of alternating Gly and Ser residues, with 12 clinker composed primarily of alternating Gly and Ser residues, with 13 clinker composed primarily of alternating Gly and Ser residues, with 14 clinker composed primarily of alternating Gly and Ser residues with 15 clinker composed primarily of alternating Gly and Ser residues with 16 clinker composed primarily of alternating Gly and Ser residues with 17 clinker composed in E.coli. Soluble, folded chain antibody (SCA) was 17 conversed in E.coli. Soluble, folded chain antibody (SCA) was 18 capable of exhibiting a biological binding activity 18 cquivalent in specificity and affinity to that of a monoclonal 18 capable of smaller size, greater stability and reduced cost.
                                                                                                                                                                                            Query Match
Best Local :
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02-SEP-1986;
02-SEP-1986;
02-SEP-1987;
19-JAN-1989;
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01-APR-1993;
06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bird RE, Hardman K, WPI; 96-333309/33. N-PSDB; T13739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single chain binding molecule 18-2-3/TRY202'.
Antibody engineering; single polypeptide chain binding single chain antibody; SCA; heavy chain; light chain; monocional antibody; MAb; immunoaffinity purification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5534621-A
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                                                                                                                     LTQSPAIMSASPGEKVIMTCSASSSVSN--MHWYQQKSSTSPKLWVYDTSKLASGVPGRF 60
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                                                    SGSGSGNSYSLTISSMEAEDAATYYCYQGSGYPFTFGSGTKLEIKGSTSGSGKSSEGKGV 120
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 QLQQSGVELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIHPENGNTVYDP 180
                                  SGGGSGTSYSLTISSVEAEDAATYYCQQYSGYPLTFGAGTKLELEGKSSGSG--SESKST
                                                                                                       LTQSPAIMSASPGEKYTMTCRASSSVSSSYLHWYQQKSGASPKLWVYGTSNLASGVPARF
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                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                of smaller size,
239 AA;
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US-902971.

US-092110.

US-299617.

US-512910.

US-512910.

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                                                                                                                                                                           29;
                                                                                                                                                                                        Score 748.5; DB 1
Pred. No. 6.7e-46;
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US4946778-A.
07-AUG-1990.
19-JAN-1989; 299617.
12-SEP-1986; US-902971.
02-SEP-1987; US-092110.
19-JAN-1989; US-299617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence was constructed from the variable regions of an antifluorescein MAb, 18-3-2, an IgM. The VL and VH cDNA sequences were synthesised by priming on RNA isolated from hybridona cells. The sequence encodes a single chain binding molecule comprising the variable regions of heavy and light chains linked by peptides. The peptide linker was computer-designed to fit inyo a groove on the backside of the variable domain structure and is composed primarly of alternating Gly and Ser residues. Glu and Lys residues see also R06476-R06484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               variable region.
Disclosure; Fig 39; 68pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single polypeptide chain binding molecules - having light chavariable region of antibody linked by peptide to heavy chain
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18-2-3-/TRY
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Ladner RC, Bi
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                                 QLQQSGVELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIHPENGNTVYDP 180
                                                                                                                                                                                                                                                                 SGSGSGNSYSLTISSMEAEDAATYYCYQGSGYPFTFGSGTKLEIKGSTSGSGKSSEGKGV 120
                                                                                                                                                                                                                                                                                                                                                      LTQSPAIMSASPGEKVNMTCRASSSVSSSYLHWYQQKSGASPKLWVYGTSNLASGVPARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             er RC, Bird RE, Hardman 90-260350/34.
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ALMSRLSISKDNSKSQVFLKMNSLQIDDTAIYYCAKRLERIFYYAMDYWGQGTSVTVS
                                                                                                                                                                                                                                      SGGGSGTSYSLTISSVEAEDAATYYCQQYSGYPLTFGAGTKLELEGKSSGSG--SESKST 122
                                                                                                                   QLKESGPVLVAPSQSLSITCTVSGFSLTNYGVHWVRQPPGKGLEWLGVIW-AGGNTNYNS 181
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61.8%;
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Pred. No. 1.3e-45;
9; Mismatches 57;
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